

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 14:34:42 ; Search time 74.81 Seconds
(Without alignments)
3473.870 Million cell updates/sec

Title:

US-09-852-845-1

Perfect score:

1058

1 cagcagagacgagatgctgc.....cacataaaccttgccag 1058

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA:*
1: /cgn2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1044.4	98.7	1057	1	US-08-147-784-1
2	1044.4	98.7	1057	4	US-08-195-367-1
3	1044.4	98.7	1057	4	US-08-472-940-1
4	814.4	77.0	848	1	US-08-192-480A-1
5	286.6	27.1	1317	1	US-08-097-827-10
6	286.6	27.1	1317	1	US-08-494-574-10
7	283.2	26.8	618	1	US-08-097-827-6
8	283.2	26.8	618	1	US-08-494-574-6
9	56	5.3	1006	3	US-08-911-423-3
10	49.4	4.7	723	3	US-08-911-423-5
11	48.8	4.6	8438	1	US-07-945-283-1
12	48.2	4.6	1632	1	US-07-959-941-1
13	48.2	4.6	1632	1	US-08-259-924-1
14	47.2	4.5	1164	2	US-08-794-796-1
15	47.2	4.5	1347	2	US-08-286-529-18
16	47.2	4.5	1859	4	US-09-286-529-19
17	45	4.3	1182	4	US-09-385-028-19
18	45	4.3	11604	4	US-09-385-028-13
19	45	4.3	15079	4	US-09-385-028-1
20	44.6	4.2	1065	4	US-08-765-907A-7
21	44.6	4.2	4496	4	US-08-765-907A-6
22	44.2	4.2	2674	4	US-09-817-180-1
23	43.6	4.1	20235	1	US-07-642-734C-3
24	43.6	4.1	20235	3	US-08-439-009A-3
25	43.4	4.1	3950	4	US-09-226-012-3
26	42.8	4.0	4257	2	US-08-690-473-1
27	42.8	4.0	4257	4	US-09-259-821A-1

C 28	42.8	4.0	4257	4	US-08-843-659-1	Sequence 1, Appl
C 29	42.8	4.0	7791	3	US-08-949-386-23	Sequence 23, Appl
C 30	42.8	4.0	7791	3	US-08-450-562-23	Sequence 23, Appl
C 31	42.8	4.0	7791	4	US-08-984-709A-23	Sequence 22, Appl
C 32	42.8	4.0	7808	3	US-08-949-386-22	Sequence 22, Appl
C 33	42.8	4.0	7808	3	US-08-450-562-22	Sequence 22, Appl
C 34	42.8	4.0	7808	3	US-08-984-709A-22	Sequence 22, Appl
C 35	42.8	4.0	12001	1	US-08-458-568A-11	Sequence 11, Appl
C 36	42.6	4.0	870	2	US-08-708-855A-4	Sequence 4, Appl
C 37	42.6	4.0	870	2	US-08-287-375-4	Sequence 4, Appl
C 38	42.6	4.0	1826	2	US-08-708-855A-14	Sequence 14, Appl
C 39	42.6	4.0	1826	3	US-09-287-375-14	Sequence 14, Appl
C 40	42.4	4.0	1724	5	PCT-US96-12374-1	Sequence 1, Appl
C 41	42	4.0	3480	4	US-09-226-012-1	Sequence 1, Appl
C 42	42	4.0	3923	3	US-08-860-635A-20	Sequence 20, Appl
C 43	42	4.0	3923	3	US-09-281-476-20	Sequence 20, Appl
C 44	41.6	3.9	1412	1	US-08-097-831-1	Sequence 1, Appl
C 45	41.6	3.9	30001	1	US-08-125-468-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-147-784-1
: Sequence 1, Application US/08147784
: Patent No. 5821332
GENERAL INFORMATION:
: APPLICANT: Godfrey, Wayne
: APPLICANT: Buck, David
: APPLICANT: Engleman, Edgar G.
: TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
: TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESS: Townsend and Townsend Kourie and Crew
: STREET: 379 Lytton Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: US
: ZIP: 94301
COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/147,784
: FILING DATE: 03-NOV-1993
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Smith, William M.
: REGISTRATION NUMBER: 30,223
: REFERENCE/DOCKET NUMBER: 05490A-220
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (415) 326-2400
: TELEFAX: (415) 326-2422
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1057 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHETICAL: NO
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 15..845
: OTHER INFORMATION: /standard_name="ACT-4 cDNA"
US-08-147-784-1
Query Match 98.7%; Score 1044.4; DB 1; Length 1057;

Best Local Similarity 99.8%; Pred. No. 3.2e-189;
Matches 1056; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

OY 1 cagcagaagacgaagatgctgtaggggctcgagcgtgagccgagcgtgctgagcgtc 60
    |||||||
DB 1 CAGCAAGAGAGAGATGCTGTGGGGCTCGGGGCTGGGGCCCGGCGCTGTGCGGCTC 60
OY 61 tgcctcctgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgt 120
    |||||||
DB 61 TGTCTCTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120
OY 121 acccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
    |||||||
DB 121 ACCCCAGCAAGAGAGATGCTGACAGAGTGCAGGCGCAGGCGAGGAGTGTAGCCGCT 180
OY 181 gcaagcgtcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 240
    |||||||
DB 181 GCAGCGCGCTCCAGAGACAGGCTGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 240
OY 241 tcaagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
    |||||||
DB 241 TCAGCTCAAGCGCTGCAAGCGCTGCAAGCGCTGCAAGCGCTGCAAGCGCTGCAAGCG 300
OY 301 agcagctgtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
    |||||||
DB 301 AGCAGCTGTGACAGGCGCACAGGACAGTGTGCGGCTGCGGCGGCGGCGGCGGCGG 360
OY 361 tgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 420
    |||||||
DB 361 TGAGACAGTACAAAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 420
OY 421 ggaagacacacagcgtcagcagcgtcagcagcgtcagcagcgtcagcagcgtcag 480
    |||||||
DB 421 GGCACAAACAGGCGCTCAAGCGCTGACCAACAGCTGTGCGGAGCAACACCTCG 480
OY 481 agcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540
    |||||||
DB 481 AGCGGCGCAGCAATAGCTGTGAGAGCAATGTGTAGAGCAAGGAGGCCCGCAGCCAG 540
OY 541 cccagagacacacagcgtcagcagcgtcagcagcgtcagcagcgtcagcagcgtcag 600
    |||||||
DB 541 CCCAGAGAGACCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 600
OY 601 ccaagacacacacagcgtcagcagcgtcagcagcgtcagcagcgtcagcagcgtcag 660
    |||||||
DB 601 CCAAGAACTTACAGGAGACCTTACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
OY 661 cgaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 720
    |||||||
DB 661 CGCGCATCTGCGGCGCTGCGGCTGTGCTGTGCGGCGCGCGCGCGCGCGCGCGCT 720
OY 721 cccctgacctgctcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 780
    |||||||
DB 721 CCTGTACTGTGCTCGGAGGAGACAGAGGCTGCGCGCGCGCGCGCGCGCGCGCG 780
OY 781 gaggcagcttcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 840
    |||||||
DB 781 GAGGCGAGTTTCCGAGCCCTATCCAGAGAGAGAGCGCCAGCTCTACCTCTGCGCA 840
OY 841 agatctgacctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 900
    |||||||
DB 841 AGATCTGAGC-10GGGCCCAAGAGTGTGAGCTGTGCGGCGCGCGCGCGCGCGCG 900
OY 901 gtcctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 960
    |||||||
DB 901 GTCTGCTGGGCGAGAGGAGGAGTGTGAGCGCGCGCGCGCGCGCGCGCGCGCGCT 960
OY 961 ctagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1020
    |||||||
DB 961 CTGACACGCTTCTAGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGT 1020
OY 1021 cctcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1056
    |||||||

```

```

DB 1020 CCTCTGCCCCCGGAGCACCAATATAAACCTTGGCAG 1057

RESULT 2
US-08-195-967-1
; Sequence 1, Application US/08195967
; Patent No. 6242566
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..845
; OTHER INFORMATION: /standard_name="ACT-4 cDNA"
US-08-195-967-1

Query Match 98.7%; Score 1044.4; DB 4; Length 1057;
Best Local Similarity 99.8%; Pred. No. 3.2e-189;
Matches 1056; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 cagcagaagacgaagatgctgtaggggctcgagcgtgagccgagcgtgctgagcgtc 60
    |||||||
DB 1 CAGCAAGAGAGAGATGCTGTGGGGCTCGGGGCTGGGGCCCGGCGCTGTGCGGCTC 60
OY 61 tgcctcctgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgtgagcgt 120
    |||||||
DB 61 TGTCTCTCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 120
OY 121 acccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
    |||||||
DB 121 ACCCCAGCAAGAGAGATGCTGACAGAGTGCAGGCGCAGGCGAGGAGTGTAGCCGCT 180
OY 181 gcaagcgtcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 240
    |||||||
DB 181 GCAGCGCGCTCCAGAGACAGGCTGTGCGGCTGCGGCTGCGGCTGCGGCTGCGGCT 240
OY 241 tcaagcctcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
    |||||||

```

```

Db 241 TCAGCTCCAAAGCCCTGGCAAGCCCTGTCAGTGTGTAACCTCAGATGAGATGAGCCGA 300
QY 301 agcagctgtgcaagcgcacacagagacagctcgcgtgcggcgagccagccccc 360
Db 301 AGCAGCTGTGACGGCCACACAGACACAGTGTGCGGCGGGGACCCACAGCCCC 360
QY 361 tggacagctaacagccttggagttgactgtgcccctgcccctccagaggaacttctccag 420
Db 361 TGGACAGCTAACAGCCTTGGAGTTGACTGTGCCCCCTGCCCCCAAGGGGACTTCTCCAG 420
QY 421 ggcagcaacacagcgtcgaagcccttgagcaactcgtcgttggaggaagcaccctg 480
Db 421 GCGCAACACCAAGCCTGCAAGCCCTGAGCAACTGCACCTTGCTGGGGAAGCACAACCTG 480
QY 481 agcggcgacagcaatagctcggagcgaactctgtgagagagagagaccccaacagcagc 540
Db 481 AGCGGCGACGCAATAGCTCGAGCCCAATCTGTAGAGAGAGGAGACCCCAACCAAGCAGC 540
QY 541 cccagagagacccagagcccccgcagccacatcactgtccagcccaactgaagcctgagc 600
Db 541 CCCAGAGAGACCCAGAGCCCGCCCGGAGCCCAATCAGTGTCCAGGCCCACTGAAGCCTG 600
QY 601 ccagaaactcaagaggaactccacacccggccgttggaggttcccgagggtccgtgctg 660
Db 601 CCAGAACTCTACAGAGGACCTTCCACCCGCGCTGTGAGGTCTCCGCGGGCGGTGGCGTTG 660
QY 661 ccgcacatcctgtgagcctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 720
Db 661 CCGCATCTGTGGGCTGTGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
QY 721 cccgtgtacactgtcctcggagagagagagagagctgtcccccagatgcccacaaagccccc 780
Db 721 CCTGTACTCTCTCGGAGGAGACAGAGAGCTGCCCGCCGATGCCCCACAAAGCCCGCTGG 780
QY 781 gagcagagtttcggagaccccccatcacaagagagagagagagagagagagagagagag 840
Db 781 GAGCAGAGTTTCCGAGACCCCATCCAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 840
QY 841 agactcagcttggagcccaacaaagtgtgaagcgtgtgcccgcagagctgtggagcccgag 900
Db 841 AGACTCAGCTG-TGGGCCACCAAGGTGAGCCTGGGCCCCCAGAGCTGTGAGAGCCGAGAG 899
QY 901 gctcgtgtgagcagagagagagagagagagagagagagagagagagagagagagag 960
Db 901 GTCTGTGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 959
QY 961 ctgacagcttctagtgctgagtgctgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 1020
Db 961 CTGACAGCTTCTTAGTGTGCGATGTGCTCGGCTCTCTCTTACGTATGCGATGACATA 1019
QY 1021 cctcctgcccgcggagacacataaaaccttggcag 1058
Db 1020 CCTCTGCCCCGCGGAGCCACATRAAAACCTTGGCAG 1057

```

RESULT 3
US-08-472-940-1
Sequence 1, Application US/08472940

Patent No. 6277962
GENERAL INFORMATION:
APPLICANT: Godfrey, Wayne
APPLICANT: Buck, David
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend Hourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301

```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,940
FILING DATE: 06-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/147,784
FILING DATE: 03-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05490A-220
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 15..845
OTHER INFORMATION: /standard_name="ACT-4 cDNA"
US-08-472-940-1

```

Query Match 98.7%; Score 1044.4; DB 4; Length 1057;
Best Local Similarity 99.8%; Pred. No. 3.2e-189;
Matches 1056; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```

QY 1 cagcagagacagagatgtgctgtgagagagctcggcggcgtgagccggcgagctgtgctgtc 60
Db 1 CAGCAGAGACAGAGATGTGTGCTGTGGGGCTCGGCGCTGGCCCGCGGCTGTGGCGCTC 60
QY 61 tgcctcctgtgagccttggagctgtgagacagctgtgagcgggtccactgtgtcgggagacact 120
Db 61 TGCTCTCTGTGGGCTGTGGGGCTGTGAGCACCCTGTGACGGGGCTCAGTGTGCGGGAGACACT 120
QY 121 acccagcagagcagcgggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
Db 121 ACCCAGCAGACGACCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
QY 181 gtagcagcttcccaagacagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 240
Db 181 GTAGCGCTTCCCAAGACAGGTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240
QY 241 tcaagctcaagcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
Db 241 TCAGCTCCAAAGCGGTGCAAGCCCTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 300
QY 301 agcagctgtgcaagcgcacacagagacagagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 360
Db 301 AGCAGCTGTGCAAGCGCCACACAGACACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 tggacagctaacagccttggagttgactgtgcccctgcccctccagaggaacttctccag 420
Db 361 TGGACAGCTAACAGCCTTGGAGTTGACTGTGCCCCCTGCCCCCAAGGGGACTTCTCCAG 420
QY 421 ggcagcaacacagcgtcgaagcccttgagcaactcgtcgttggaggaagcaccctg 480
Db 421 GCGCAACACCAAGCCTGCAAGCCCTGAGCAACTGCACCTTGCTGGGGAAGCACAACCTG 480
QY 481 agcggcgacagcaatagctcggagcgaactctgtgagagagagagagagagagagagagag 540
Db 481 AGCGGCGACGCAATAGCTCGAGCCCAATCTGTAGAGAGAGGAGACCCCAACCAAGCAGC 540

```

```

Qy 541 cccagagagacccagggcccccccgccagggcccaatcactgtccagccacttgaagcctggc 600
    |||||||
Db 541 cccagagagacccagggcccccccgccagggcccaatcactgtccagccacttgaagcctggc 600
Qy 601 ccaagaacctcaagaggaacctccacccggccgttgaaggtcccccgggggagcgttggcttg 660
    |||||||
Db 601 ccaagaacctcaagaggaacctccacccggccgttgaaggtcccccgggggagcgttggcttg 660
Qy 661 ccagcaatcctggagcctggagcctgtgtgtggagctgtgtggagcctccctggagccttctgtg 720
    |||||||
Db 661 ccagcaatcctggagcctggagcctgtgtgtggagctgtgtggagcctccctggagccttctgtg 720
Qy 721 cccctgtacctgtctcggagggaggaagagctgtgcccccgatggcccaagcccccttgggg 780
    |||||||
Db 721 cccctgtacctgtctcggagggaggaagagctgtgcccccgatggcccaagcccccttgggg 780
Qy 781 gaggagcagttccggagcccccatccaaagagagagagcagagccacactccacacttggcca 840
    |||||||
Db 781 gaggagcagttccggagcccccatccaaagagagagagcagagccacactccacacttggcca 840
Qy 841 agatcagcagcttggagcccaagagtgagagctgtggcccccgacagagcttgaagcccgagag 900
    |||||||
Db 841 agatcagcagcttggagcccaagagtgagagctgtggcccccgacagagcttgaagcccgagag 900
Qy 901 gtctctgtggcgagagcagagcagagtgacagagccgctgcccccgacagagcttctggagcaact 960
    |||||||
Db 901 gtctctgtggcgagagcagagcagagtgacagagccgctgcccccgacagagcttctggagcaact 960
Qy 961 ctgagagcgttcttaagtgctcgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
    |||||||
Db 961 ctgagagcgttcttaagtgctcgagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1020
Qy 1021 cctctctgcccccgaggagacacaaataaaaaacttggcag 1058
    |||||||
Db 1021 cctctctgcccccgaggagacacaaataaaaaacttggcag 1058
Qy 1020 cctctctgcccccgaggagacacaaataaaaaacttggcag 1057
    |||||||

```

```

TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (503) 226-7391
; TELEFAX: (503) 228-9446
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 848 base pairs
; TYPE: Nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: Linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
;
US-08-192-480A-1

Query Match      77.0%; Score 814.4; DB 1: Length 848;
Best Local Similarity 97.5%; Pred. No. 7.9e-146;
Matches 827; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

Qy 1 cagcagagacgagagatgtcgttggggctcgcgcgttgggcccgggcccgtgtgcgctc 60
    |||||||
Db 1 cgcagagagacgagagatgtcgttggggctcgcgcgttgggcccgggcccgtgtgcgctc 60
Qy 61 tgcctctctgggcccgtggggctgaagcagcgttgaaggggtccactgtgtcggggaacct 120
    |||||||
Db 61 tgcctctctgggcccgtggggctgaagcagcgttgaaggggtccactgtgtcggggaacct 120
Qy 121 acccagagacagacgagctgtgcagagatgtcagagcagagcaagaggaatgtatgagccgt 180
    |||||||
Db 121 acccagagacagacgagctgtgcagagatgtcagagcagagcaagaggaatgtatgagccgt 180
Qy 181 gcaagcgcctccagaaacagagtgctgcgttcgtgcgggcccgggtctctacaacagacgtg 240
    |||||||
Db 181 gcaagcgcctccagaaacagagtgctgcgttcgtgcgggcccgggtctctacaacagacgtg 240
Qy 241 tcaagctcgaagcgtgtgaagccttgcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
    |||||||
Db 241 tcaagctcgaagcgtgtgaagccttgcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
Qy 301 agcagctgtgcaagcgcgcacacagagacagatctgcgcgttgcgggcccgggcaaccagcccc 360
    |||||||
Db 301 agcagctgtgcaagcgcgcacacagagacagatctgcgcgttgcgggcccgggcaaccagcccc 360
Qy 361 tggagcagctacaagccttgaagtgactgtgtgccttgcctccctccagaggaacttctccag 420
    |||||||
Db 361 tggagcagctacaagccttgaagtgactgtgtgccttgcctccctccagaggaacttctccag 420
Qy 421 ggcagacacagagccttgaagccttgcagcaactgtgcaactgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
    |||||||
Db 421 ggcagacacagagccttgaagccttgcagcaactgtgcaactgtgtgtgtgtgtgtgtgtgtgtgtgtgt 480
Qy 481 agcagcagcagcaataagctcggagcgaatctgttgaagacagagagccccccagccagcagc 540
    |||||||
Db 481 agcagcagcagcaataagctcggagcgaatctgttgaagacagagagccccccagccagcagc 540
Qy 541 agccggccagatattagctgtgagacgaatgtgtgaggaacagagccccccagccagcagc 540
    |||||||
Db 541 agccggccagatattagctgtgagacgaatgtgtgaggaacagagccccccagccagcagc 540
Qy 541 cccagagagacccagggcccccccgccagggcccaatcactgtccagccacttgaagcctggc 600
    |||||||
Db 541 cccagagagacccagggcccccccgccagggcccaatcactgtccagccacttgaagcctggc 600
Qy 601 ccagaacctcaagaggaacctccacccggccgttgaaggtcccccgggggagcgttggcttg 660
    |||||||
Db 601 ccagaacctcaagaggaacctccacccggccgttgaaggtcccccgggggagcgttggcttg 660
Qy 661 ccagcaatcctggagcctggagcctgtgtgtggagctgtgtggagcctccctggagccttctgtg 720
    |||||||
Db 661 ccagcaatcctggagcctggagcctgtgtgtggagctgtgtggagcctccctggagccttctgtg 720
Qy 721 cccctgtacctgtctcggagggaggaagagctgtgcccccgatggcccaagcccccttgggg 780
    |||||||
Db 721 cccctgtacctgtctcggagggaggaagagctgtgcccccgatggcccaagcccccttgggg 780
Qy 781 gaggagcagttccggagcccccatccaaagagagagagcagagccacactccacacttggcca 840
    |||||||

```

Db 781 GAGGAGCTCCGACGCCCATCCAGAGACGAGCCGACGCCCATCTGATGCA 840
Qy 841 agatctga 848
Db 841 AGTCTGA 848

RESULT 5
US-08-097-827-10
Sequence 10, Application US/08097827
GENERAL INFORMATION:
APPLICANT: Baum, Peter
Goodwin, Ray
Faslow, William
Gayle, Richard
TITLE OF INVENTION: Novel Cytokine which is a Ligand for
OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-Jul-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MOX40Fc Mutein
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1317
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-097-827-10

Query Match 27.1%; Score 286.6; DB 1; Length 1317;
Best Local Similarity 66.6%; Pred. No. 3e-46;
Matches 428; Conservative 0; Mismatches 209; Indels 6; Gaps 1;

Qy 87 accgtgacggggctccacctgtgtcggggacacctaacccagcaaacggtgtgtcacac 146
Db 61 ACAGCAAGCGGCTCAACTGTGTTAAACATACCTACCCAGGGTCAACAAGCTGTCTGT 120
Qy 147 gattgcagagcagcaacggaattgtgagccgtgtcagccgtctcccaagaacaggtgtgc 206
Db 121 GATGTCCAGCCAGGCGCATGATGTGAACCGCTGTGATCATACCAAGGATATCTATGT 180
Qy 207 cgtccgtgcggcgccgggtcttctaacagagactgtgtcagctcacaagcgttcaagccctgc 266

Db 181 CATCCGTGAGACATGGCTTTTACAATGAAGCTGTCAATTATGATACCTGACAGCAGTGT 240
Qy 267 acgtgtgttaacctcaagaagtgtgagtgagcggaagcaactgtgtcagggccacaagaagc 326
Db 241 ACACAGTGCACACCATTCGAGTGAAGTGAACCAACGACAAATTTGACACACTCTCAGCAT 300
Qy 327 acagctgcgcctgtcccgcggaaccccgcccttggga-----cagctcaagcttga 380
Db 301 ACTGTCTGCAGATGTAGACACGACGACACCACTCCGAGAGACAGCGGCTTCAAGCTTGA 360
Qy 381 gttgaactgtccccctgtccctcccaaggcaactctctcccaaggcgaacacgaagcctgtcaag 440
Db 361 GTTGACTGTGTCTCCCTGCCCTCTGTGCTCTCTGAGCAACACCAAGCGCTGTGAAG 420
Qy 441 cccctgaccgaactgtcaactgtgtgtgtgtggaagacacccctgtcagccggtcagaatagtctg 500
Db 421 CCTGTGACCAATTTGATCTTATCTGAAGCGAGACCCCGCACCCGACGATGACAGCTTG 480
Qy 501 gacgaatctgtgagagacagggagcccccagcagcagcagcaggaagacccagggccc 560
Db 481 GACGCACTGTGTGAGAGACAGAGCCTTCTGCGCACACTGCTGTGGAGACCCAGCGCCT 540
Qy 561 ccggcagggcccaactactgtccagcccaactgaagcctgtgcccagaaactacagggagacc 620
Db 541 ACATTGAGGCCAACCACTGTCCATTCACACACAGTCTGTGCGCCAGAGACTTGTAGTTGCC 600
Qy 621 tccaccggcccggtgaggtgtcccgggggcggtgcggtgtgcacatctgtggtgtgac 680
Db 601 TCTACACCCACTTGTGTGAGGCCAGATCTTGTGCAAAATCTACACATGCCACCGCTGC 660
Qy 681 ctgtgtcgtgggctgtgtgccccctgtggccatccctgtgccc 723
Db 661 CCAGCACTGAGAGCGGAGGCGCGCTCAGTCTTCTCTCTCC 703

RESULT 6
US-08-494-574-10
Sequence 10, Application US/08494574
Patent No. 5783655
GENERAL INFORMATION:
APPLICANT: Baum, Peter
Goodwin, Ray
Faslow, William
Gayle, Richard
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 10:

```

? SEQUENCE CHARACTERISTICS:
? LENGTH: 1317 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? IMMEDIATE SOURCE:
? CLONE: M0X4DFc MuteIn
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..1317
US-08-494574-10

```

Query Match	27.1%	Score 285.6	DB 1	Length 1317
Best Local Similarity	66.6%	Pred. No. 3e-46		
Matches 428	Conservative	0	Mismatches 209	Indels 6
				Gaps 1

Oy	87	acttgaagggggtcccaactgtgtctggggaacacccaacccaagcaagacggtgtctgcac	146
Db	61	ACACGACGGGGCTCMACTGTGTAAACATACCTACCCCAAGTGTCACAAGTCTGTCT	120
Oy	147	gaatgaagcccaagcaacggaatgtgtagccgctgtcaagccgctcccaagaacagttgtgc	206
Db	121	GAGTGCCAGCCAGGCCCATGTGATGTGAACCGCGTGTATCATACAGGGATACTTATGT	180
Oy	207	cgctccgtbpcgggcccgggctcttaaaagaagttgttagctccaagccggtgtcaagccctgc	266
Db	181	CATCGGTGTGAAGTGGCTTTACAAATGAAGCTGTCAATTATGTATCTTCAAGCAAGTGT	240
Oy	267	aagttgtgtaaacctcaagaagtgtggaagtgtgacggaagacgtgtgtcagcgcacacagagac	326
Db	241	ACACAGTGCACATCGAAGTGAAGTGAAGTCAAGCAAGATTTGACACTACTCAGGAT	300
Oy	327	acgaatctgcgcgtctccggggcgagcaaccaagcccttga-----cagctcaagccttga	380
Db	301	ACTGTCTGCAATGTAGACCGAGGACCCCAACCTGTGGCAGGACAGCCGGCTTCAAGCTTGA	360
Oy	381	gttgaactgtgccctctccctccagaagcaactctctccagaagcgaacaaacagagcctcaag	440
Db	361	GTTGACTGTGTCCCTGCTCCCTCCTGTGGCACTTTTCTCAGGCAACAAACGCGCTGCAG	420
Oy	441	cccttgaacaaactgtcaccttgcgtctggaagacacaccccttgacgcggcgcaagaaatagctgc	500
Db	421	CCCTGGACCAATTTGACTTATCTGGAAGAGACCCGCCACCCAGCCAGCACTGACAGTTG	480
Oy	501	gaagcaaatctgttgagagaaggaagacccccagccagccagcccccagaggaacccaagggcccc	560
Db	481	GAGCGAAGCTTGTGAGAGAGAAAGCCTCTTGCCCACTGTCTTGGGAGACCCAGCGCCT	540
Oy	561	ccggccagggcccaactcaactgtctcagcccaatgaagcctcgggcccagaacactcaagggagccc	620
Db	541	ACATTCAAGGCCAACCACTGTCTCATTCACACAGACTCTGGCCCAAGACTTCTGAAGTTGCC	600
Oy	621	tccaacccggcccgttggagatcccccgggggcccgttgcgtgtgcgcgcacatccttgggccttgcg	680
Db	601	TCTACACCCACACTTGTGTGAGACCCAGATCTTGTGACAAAAATCACACATGCCACCGCTGC	660
Oy	681	ctgtgtgcgtggggcgtctcttgggcccctctggccaatcctgtgtggccc	723
Db	661	CCAGCACCTGAAGCCGAGGGCGGCCCGTCAAGTCTTCTCTTCC	703

RESULT 7
US-08-097-827-6
; Sequence 6, Application US/08097827

```

1  TITLE OF INVENTION: Novel Cytokine Which is a Ligand for
2  OX40
3  NUMBER OF SEQUENCES: 13
4  CORRESPONDENCE ADDRESS:
5  ADDRESSEE: Immunex Corporation
6  STREET: 51 University Street
7  CITY: Seattle
8  STATE: WA
9  COUNTRY: USA
10 ZIP: 98101
11
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: Patent In Release #1.0, Version #1.25
17
18 CURRENT APPLICATION DATA:
19 APPLICATION NUMBER: US/08/097,827
20 FILING DATE: 23-Jul-1993
21 CLASSIFICATION: <Unknown>
22
23 ATTORNEY/AGENT INFORMATION:
24 NAME: Perkins, Patricia A.
25 REGISTRATION NUMBER: 34,693
26 REFERENCE/DOCKET NUMBER: 2806
27
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 206-587-0730
30
31 INFORMATION FOR SEQ. ID NO: 6:
32
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 618 base pairs
35 TYPE: nucleic acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: cDNA to mRNA
39
40 HYPOTHETICAL: NO
41 ANTI-SENSE: NO
42 IMMEDIATE SOURCE:
43 CLONE: MOUSE OX40
44
45 FEATURE:
46 NAME/KEY: CDS
47 LOCATION: 1..618
48
49 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
50
51 US-08-097-827-6

```

Query Match	26.8%	Score 283.2	DB 1	Length 618
Best Local Similarity	70.6%	Pred. No. 1.3e-45		
Matches 394	Conservative	0	Mismatches 158	Indels
				Gaps 6
Qy	accgctgacagggctccactctgctcgaggagacacctccacgaacagcgctgctccac	146		
Db	61 ACAGCAGGCGGCTCAACTGTTTAAACATACCTACCTCCAGTGGTCAAAAGTGGTCTGT	120		
Qy	147 gagctcagagcgagcaacgggaatgltgaacgctgacgctcccaagaacaggtgtgc	206		
Db	121 GAGTGCCAGCCAGGCGCATGTGTGTGTGAACCGCTGTGATCATACGAGGATACCTATGT	180		
Qy	207 cgtccgtccgggacgggctctctacaagaagtgtgcagctccaaagcgtgtgaagccctgc	266		
Db	181 CATCCGTGTGAACACGCGTTCTTACATATGAAGCTGTCAATTATGTAACTCGGAAGCAGTGT	240		
Qy	267 acgtgtgttaacctcagaagtgtgaggtgtagcggaagcagcgtgtgcacggccacagagac	326		
Db	241 ACACAGTGCACACCATTCGAAGTGAAGTGAATCAACGCAAGAAATTGCACACCTTACTAGGAT	300		
Qy	327 acagcttcgcgcgtcgcgggacggccacccgcctctgga-----cagctacaagcgtgta	380		
Db	301 ACTGCTCGCAGATGTATGAACACAGCACCACTCGGACAGACAGGCGCTTACAGCTTGA	360		
Qy	381 gltgacgtgtgccccctgcctccacaggaactctctccagagcgacaacacaggtctgcaag	440		
Db	361 GTTGAAGTGTGTTCCCTGCCCTCTCGCCACACTTTTCTCCAGGCAACACAGGCGCTGCAAG	420		
Qy	441 cccctgaccacactgcaacttggctctggtgaagacacacccctgacggcgcgacaaatagctcg	500		

Matches 394; Conservative 0; Mismatches 158; Indels 6; Gaps 1;

;; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027,901


```
SEQUENCE CHARACTERISTICS:
LENGTH: 8438 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Pseudorabies virus
FEATURE:
NAME/KEY: CDS
LOCATION: 622..6495
FEATURE:
NAME/KEY: variation
LOCATION: replace(1099, "g")
FEATURE:
NAME/KEY: variation
LOCATION: replace(1267, "t")
FEATURE:
NAME/KEY: variation
LOCATION: replace(1381, "c")
FEATURE:
NAME/KEY: variation
LOCATION: replace(1566, "c")
FEATURE:
NAME/KEY: variation
LOCATION: replace(7010, "g")
US-07-945-283-1
```

```
Query Match 4.6%; Score 48.8; DB 1; Length 8438;
Best Local Similarity 47.1%; Pred. No. 0.24;
Matches 181; Conservative 0; Mismatches 202; Indels 1; Gaps 1;

QY 598 gggccagaaactcaagagaccctccaccggccgtgaggtcccgaggggcgctgcgg 657
Db 5556 gccccactgcggccggccggccggccggccggccggccggccggccggccggccgg 5497

QY 658 ttgcgcacatcctgggcctgggcctgctgctggggcctgctgggcctgacatcgc 717
Db 5496 cccctgcgcctcctccgctccgctccgctccgctccgctccgctccgctccgctcc 5437

QY 718 tggccctgactcgtcctcgagagagagagagagagagagagagagagagagagag 777
Db 5436 cggagagccggccggccggccggccggccggccggccggccggccggccggccgg 5377

QY 778 gggagagagagagagagagagagagagagagagagagagagagagagagagagag 837
Db 5376 atggccgagagagagagagagagagagagagagagagagagagagagagagagag 5317

QY 838 caaagatgagagagagagagagagagagagagagagagagagagagagagagagag 896
Db 5316 cccggctccgagagagagagagagagagagagagagagagagagagagagagagag 5257

QY 897 gaggagctgctgagagagagagagagagagagagagagagagagagagagagagag 956
Db 5256 gagggagctctggagagagagagagagagagagagagagagagagagagagagag 5197

QY 957 aactctgacagctctctagtgccg 980
Db 5196 gggcccgctggccggctgctgctgctg 5173
```

```
RESULT 12
US-07-959-941-1
Sequence 1, Application US/07959941
Patent No. 5364/81
GENERAL INFORMATION:
APPLICANT: HUTCHINSON, Charles R.
APPLICANT: MADURRI, Krishna M.
APPLICANT: TORRI, Francesca
APPLICANT: COLOMBO, Anna L.
```

```
TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaibo, Marmelstein, Murray & Oram
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,941
FILING DATE: 19921009
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 793,873
FILING DATE: 18-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Chin, Monica F.
REGISTRATION NUMBER: P-36,105
REFERENCE/DOCKET NUMBER: 1615-1816CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1632 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 204..1271
US-07-959-941-1
```

```
Query Match 4.6%; Score 48.2; DB 1; Length 1632;
Best Local Similarity 48.8%; Pred. No. 0.29;
Matches 187; Conservative 0; Mismatches 193; Indels 3; Gaps 2;

QY 655 cggctgcgcacatcctgagcctgggcctgctgctgaggtcgtgagccctggccatcc 714
Db 220 cggctgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 279

QY 715 tgcctgacctgactcgtcctcgagagagagagagagagagagagagagagagagagag 774
Db 280 tgcacacccacatgctgctcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 339

QY 775 ctggggagagagagagagagagagagagagagagagagagagagagagagagagag 832
Db 340 cggggggccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 399

QY 833 cctggcagagatcagccttggggccaccagagagagagagagagagagagagagagag 891
Db 400 tgcgactatccgcacactggtggagatgcgactctcgagagagagagagagagagag 459

QY 892 gcccgagagagagagagagagagagagagagagagagagagagagagagagagagag 951
Db 460 tgcgtccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 519

QY 952 gggccaaactctgacagctctagtgccagatgagctgctcggcgtctctgcttactatg 1011
Db 520 gccacagacctgacagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 579

QY 1012 ccatgataactcctgcccgcgg 1034
Db 580 ccattcgtacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 602
```

```

RESULT 13
US-08-259-924-1
; Sequence 1, Application US/08259924
; Patent No. 5563064
; GENERAL INFORMATION:
; APPLICANT: HUTCHINSON, Charles R.
; APPLICANT: MADURU, Krishna M.
; APPLICANT: TORI, Francesca
; APPLICANT: COLOMBO, Anna L.
; TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikolaide, Marmelstein, Murray & Oram
; STREET: 655 Fifteenth Street N.W. Suite 330
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/259,924
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 793,873
; FILING DATE: 18-NOV-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,941
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Kilts, Monica C.
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: 1615-4003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)638-5000
; TELEFAX: (202)638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1632 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 204..1271
; US-08-259-924-1

Query Match          4.6%; Score 48.2; DB 1; Length 1632;
Best Local Similarity 48.8%; Pred. No. 0.29;
Matches 187; Conservative 0; Mismatches 193; Indels 3; Gaps 2.

Oy      655 cggttgacgcgaatctctggagccctgggcccgttgctggtggttggcccccgcccatc 714
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      220 CGGTGCGGGCCCGGCGGACGATGAGACGCCCTTAGGACCCTGTATCCGCCTGGAAAGCC 279

Oy      715 tgcctgcccctgtactctgcttcgagagagaccaggctgcccccgatgtccacaagcccc 774
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      280 TGCACACCCCATGTCGTCTCGGAGGCGCCGCCACCTGTGGGTCTGTGAACACATCTGG 339

Oy      775 ctgagggaagcaagtlctcgagacc--ccattccaagagagcaggccgacgcccattccaa 832
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      340 CCGGGGCCCCGCAACCGTGAAGGCCCTGTGGCGCCAGAGACAACACCCGGCGAAGCATTCC 399

Oy      833 ccctggcagaagtctcactcttgggcccacacaagytgtgaagcttg-ggccccgaagcttga 891
        ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      400 TCGCCTCATATCCGACCATCTGTGTGGGATTCGACTCTCGAGGAGGACGATCCGGGCGACT 459

```

```

QY      892  gcccgagagctctgctggcgagcgagggaggtgtgaagcgccctgcccgcacgctct 951
Db      460  TGTGTCCCGACCGAGGTCGGCGAGCTGCTGCCGACGACCAACCAGCCGCGACGGCT 519
QY      952  gggcacaactctgacacgttctagtgagcgatgtctgcctcgctctctctgcttaagta 1011
Db      520  GGCACGACTGTACGCGAGGCGCTGGGCGCGCGACATCTCTTCAACCGCGCTTCCCGAGC 579
QY      1012  ccattcataactctctgcccgcg 1034
Db      580  CCATCGTACCGCGCGCCCGCACG 602

RESULT 14
US-08-794-796-1
Sequence 1, Application US/08794796
Patent No. 5885800
GENERAL INFORMATION:
APPLICANT: Emery, John
APPLICANT: Tan, KB
APPLICANT: Truneh, Alem
APPLICANT: Young, Peter
TITLE OF INVENTION: Tumor Necrosis Related Receptor,
TITLE OF INVENTION: TR4
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,796
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
FILING DATE:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-794-796-1

Query Match          4.5%; Score 47.2; DB 2; Length 1164;
Best Local Similarity 46.4%; Pred. No. 0.43;
Matches 154; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY      19  gctgtgagggcgtcgagggcgtgagcgcgagggccgtgtgagcgctctgtcctcctgggacctgg 78
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      133  GCGTGTGCGTGTGTCGCGTGCGTGTCGGGCGTGCCTGCGCTGTGCGCGTGCGGCGGTATC 192
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

QY      79  gactgagcagcgtgtgacgggggtccacgtgtgtcggggacaacctaccacgaagacgggt 138
          |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

```

```
Db 193 GCGGAGTGGCAGAAACACCCACTACCCCTGGGGGACGACGAGACAGGGGAGCGGCTGG 252
QY 139 gctgcacagagtgacagcgaagcgaagatggtgagccgtgacccgctccacagaaca 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 253 TGTGGGCCCCAGTGGCCCCCAGGACACTTGTGACAGCGGCGCGTCCGCGGAGACAGCCCCA 312
QY 199 cgtgtgcgcgtcgttgcggccgggcttctacaacgacgtgtgacgtccaaagccgtga 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 313 CGAGGTGTGGCCGCTGTCCACCGCGCTACACGCACTGTGAACTACTGTGAGCGCT 372
QY 259 agccctgacgtgtgtactcctcagaatggtgagtgagcgaagcagctgtgacagcca 318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 373 GCCGCTACTGCAACCTCTCTGTGGGGGAGCGGTGAGGAGGACAGGCGCTTGCCACGCCA 432
QY 319 cacaggaacagctgcccgtgcccggcgagc 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 433 CCCACAAACCGTGGCTGGCGGCTGGCGCACCGGC 464

RESULT 15
US-09-286-529-18
; Sequence 18, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/286,529
; CURRENT FILING DATE: 1999-04-05
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 18
; LENGTH: 1347
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-286-529-18
```

```
Query Match 4.5%; Score 47.2; DB 4; Length 1347;
Best Local Similarity 46.4%; Pred. No. 0.44;
Matches 154; Conservative 0; Mismatches 178; Indels 0; Gaps 0;

QY 19 gctgtgggggctgcgcgctggtgcggcgctgtgcgctctctctctctctggtgctg 78
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 340 gctgtgcgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 399
QY 79 ggttgagcaccgtgacgggggtctccactgtgtcgggggacactaccacagcaacgacgt 138
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 gctgagatgtgcagaacacaccactacccttggtggtgacgacagagggagcgctg 459
QY 139 gctgcacagatgcagcgaagcgaagatggtgagccgtgacccgctccacagaaca 198
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 tgtgcgccagtgccccccagacacttgtgacagcggcggtgcccgcgagacagcccca 519
QY 199 cgtgtgcgcgtcgttgcggccgggcttctacaacgacgtgtgacgtccaaagccgtga 258
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 cgaagtggtgcccgtgtccacgcgcacactacagcagctctggaactaccctggaagcgt 579
QY 259 agccctgacgtgtgtactcctcagaatggtgagtgagcgaagcagctgtgacagcca 318
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 580 gctgactatgcaacgtctctgtcggtgagcgttgagagagagacagcgcttgcaagcca 639
QY 319 cacaggaacagctgcccgtgcccggcgagc 350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 640 cccacaaccgtgctgcgtgcgtgcgcgacgcgc 671
```

Search completed: June 18, 2002, 17:24:04
Job time: 10162 sec

THIS PAGE BLANK (uspto)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:23:57 ; Search time 17.68 Seconds
(without alignments)
1505.472 Million cell updates/sec

Title: US-09-852-845-2

Perfect score: 1538

Sequence: 1 MCVGARRLRGRCPCALLLLG.....SFRTPRQEQADAHSTLAKI 277

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : PIR-71:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1538	100.0	277	2	137552
2	864.5	56.2	271	2	S12783
3	857	55.7	272	2	I48700
4	224.5	14.6	427	1	GOHUN
5	221.5	14.4	277	2	A60771
6	217	14.1	461	1	A35356
7	216	14.0	425	1	A26431
8	211.5	13.8	416	1	JN0006
9	209.5	13.6	435	2	I54182
10	209	13.6	305	2	A46476
11	202.5	13.2	256	2	B32393
12	202.5	13.2	474	2	B38634
13	201.5	13.1	459	2	I48854
14	186.5	12.1	255	2	I38426
15	172	11.2	461	1	GOH71
16	171	11.1	327	2	A6484
17	168.5	11.0	651	2	JC7705
18	161	10.5	454	1	GOMST1
19	160.5	10.4	325	2	B43692
20	152	9.9	326	1	GOVZML
21	149.5	9.7	260	1	A46517
22	147.5	9.6	324	2	JC2395
23	147	9.6	595	2	A42086
24	146.5	9.5	348	2	T28623
25	146.5	9.5	349	2	D36858
26	145.5	9.5	349	2	D72175
27	144	9.4	461	2	JC4302
28	142	9.2	250	1	A49033
29	139	9.0	3075	2	S14458

30	138	9.0	1798	2	S53869	laminin beta-2 cha
31	132	8.6	1801	1	MMRTS	laminin beta-2 cha
32	128.5	8.4	1713	2	A55347	adhesive ligand ep
33	128	8.3	3635	2	T10053	laminin alpha 5 ch
34	127.5	8.3	3707	2	S18252	heparan sulfate pr
35	127	8.3	1808	2	T15099	hypothetical prote
36	126.5	8.2	3106	1	S53868	laminin alpha-2 ch
37	126	8.2	1797	2	A55677	laminin beta-2 cha
38	126	8.2	4391	2	A38096	perlecan precursor
39	125.5	8.2	722	2	I48324	DETRA-like 1 - mou
40	125	8.1	1557	2	T28811	hypothetical prote
41	124.5	8.1	455	1	GOH71	tumor necrosis fac
42	122.5	8.0	1111	2	T26972	hypothetical prote
43	122.5	8.0	1254	2	I48161	p-185 precursor -
44	122	7.9	3672	2	T23433	hypothetical prote
45	122	7.9	3704	2	T37316	probable laminin a

ALIGNMENTS

RESULT 1
137552
OX40 homolog - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
C:Accession: 137552
R:Latza, U.; Durkop, H.; Schnitger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo
Eur. J. Immunol. 24, 677-683, 1994
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen
A:Reference number: 137552; MUID:94170844
A:Accession: 137552
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <RES>
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CAAS3576.1; PID:9472958
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 100.0%; Score 1538; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 5e-94;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MCVGARRLRGRCPCALLLLGLSTVYTGHCVDTPPSNDRCHCRPGNGVSRCSNQ	60
DB	1	MCVGARRLRGRCPCALLLLGLSTVYTGHCVDTPPSNDRCHCRPGNGVSRCSNQ	60
QY	61	NTVCARPCGPGFYNDVSSKPKCKTWCNLRSGSERKOLCTATQDTPVCRACRAGTOPLDSYK	120
DB	61	NTVCARPCGPGFYNDVSSKPKCKTWCNLRSGSERKOLCTATQDTPVCRACRAGTOPLDSYK	120
QY	121	PCVDCAPCPGPHFSPGDNACKPWTNCTLAGHTLQDPAISSSDAICEDRDPATPOETQ	180
DB	121	PCVDCAPCPGPHFSPGDNACKPWTNCTLAGHTLQDPAISSSDAICEDRDPATPOETQ	180
QY	181	GPPARPTVQPTPEAMPRTSQGSPTRVEVGGRAVAALIGLVLGLPLAILATLYL	240
DB	181	GPPARPTVQPTPEAMPRTSQGSPTRVEVGGRAVAALIGLVLGLPLAILATLYL	240
QY	241	RRDQRLPPDAHNRPCGSGSFRTPRQEQADAHSTLAKI	277
DB	241	RRDQRLPPDAHNRPCGSGSFRTPRQEQADAHSTLAKI	277

RESULT 2
S12783
OX40 antigen precursor - rat
N:Alternate names: nerve growth factor receptor homolog
C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Mallett, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990

F:29-427/Product: nerve growth factor receptor #status experimental <MAT>
 F:29-250/Domain: extracellular #status predicted <EXT>
 F:32-65/Domain: NGF receptor repeat homology <NG1>
 F:67-108/Domain: NGF receptor repeat homology <NG2>
 F:109-147/Domain: NGF receptor repeat homology <NG3>
 F:149-189/Domain: NGF receptor repeat homology <NG4>
 F:197-248/Region: serine/threonine-rich
 F:251-272/Domain: transmembrane #status predicted <TRM>
 F:273-427/Domain: intracellular #status predicted <INT>
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.6%; Score 224.5; DB 1; Length 427;
 Best Local Similarity 30.1%; Pred. No. 8.4e-08;
 Matches 84; Conservative 31; Mismatches 95; Indels 69; Gaps 16;
 QY 3 VGARRLR---CP-CAALLLLGLG-----STVGLHGVGTYSNDCCHECRGNAMV 53
 Db 1 MGAGATGPRAMDGPRLLLLLGLVSLGAKKCAPTGL-----YTHSGCCACNLGEGVA 54
 QY 54 SRCRSQNTVCRPCGPFGF-VNDVVS-SKRCRPTWC-NLRSGSERKQLCTADTVCR-- 108
 Db 55 QPCANQ-TVCEPCLDSTFSDVVSATPECKPCTECVGLQSMAP---CVLEADAVCRCA 110
 QY 109 -----CRAGTQPLDSY--KPGVDCAPCPHSPGDNQA--CKPWTNC 147
 Db 111 YGYQDETTCRCACRCVCEAGSLVFSCQDKQNTVCECGPGQTSDEANHVDPCLPCTVVC 170
 QY 148 TLAKRHLLQPAKSSSDAICED-----RDPPATQPOETGPPAPRPTVQTE 193
 Db 171 E-DTERDLRECTRWADACEIPGRMTTRSTPPEGSDSTASPTOEPAPEPDDL-IASTV 228
 QY 194 AMPRTSGPSTRPYE-----VPGGRAVAAILGLGLV 224
 Db 229 AGVYTVWGSSQPVYTRGTNTNLIPVYSILAAVVGVL 267

RESULT 5
 A60771
 B-cell activation protein CD40 precursor - human
 N:Alternate names: B-cell surface antigen Bp50
 C:Species: Homo sapiens (man)
 C>Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 21-Jul-2000
 C:Accession: S04460; A60771
 R:Stamenkovic, I.; Clark, E.A.; Seed, B.
 EMBL J. 8, 1403-1410, 1989
 A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor
 A:Reference number: S04460; MUID:8935608
 A:Accession: S04460
 A:Molecule type: mRNA
 A:Residues: 1-277 <ST>
 A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851
 R:Braesch-Andersen, S.; Paulie, S.; Kono, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-11k
 A:Reference number: A60771; MUID:89093941
 A:Accession: A60771
 A:Molecule type: protein
 A:Residues: 21-50 <BRA>
 A:Experimental source: Burkitt lymphoma cell line Raji
 C:Genetics:
 A:Gene: GDB:CD40
 A:Cross-references: GDB:215268; OMIM:109535
 A:Map position: 20q12-20q13.2
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein
 F:1-20/Domain: signal sequence #status predicted <SIG>
 F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
 F:21-193/Domain: extracellular #status predicted <EXT>
 F:194-215/Domain: transmembrane #status predicted <TRM>
 F:216-277/Domain: intracellular #status predicted <CYT>
 F:153,160/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.4%; Score 221.5; DB 2; Length 277;
 Best Local Similarity 23.2%; Pred. No. 9.1e-08;
 Matches 66; Conservative 34; Mismatches 95; Indels 89; Gaps 10;

QY 26 VTGLH-----CVGDTYSNDRCHECRPGNGVSRCSQNTVCRPCGPGFYNDVSSK 79
 Db 15 LTAHVPEPPTACREKQYILNQCSCSLCPGOKLVSDCTEFTETCLPCGESEFLDTWNR 74
 QY 80 P-CKRPTWCNLRSGSERKQLCTAQTQTVCRGRAGQPLD-----SVKPGVD----- 124
 Db 75 THCHOHKTCDPNLGLRVQOKGTSETDTICTCEEGHCTSEACESCVLHRSQSPGCVKQI 134
 QY 125 -----CAPCPHGFSPGDN--QACKPWTNCTLAGKHTLQPAKSSSDAICEDDPAPT 174
 Db 135 ATGVSDTICEPCPCPVGFENSSAFKCHPWTSCERKDLVQOAGKTKDYVC----- 186
 QY 175 QPOETGPPAPRPTVQTEAMPRTSGPSTRPYEVPGGRAVAAILGLGLVGLLPLAIL 234
 Db 187 -----GPQDR-----LRALVVIPIRGIL--FAIL 209
 QY 225 LALYLRRDRLP-----PDAHKRP-----GGGSFRTPIQE 265
 Db 210 LVLFVIRKVRKPTNKAPRKOEPQELNFPDDLPGSNTAAPVQE 253

RESULT 6
 A35356
 Tumor necrosis factor receptor 2 precursor [validated] - human
 N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2
 C:Species: Homo sapiens (man)
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 08-Dec-2000
 C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094
 R:Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, Science 248, 1019-1023, 1990
 A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a
 A:Reference number: A35356; MUID:90260639
 A:Accession: A35356
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <SMT>
 A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squit
 Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc
 A:Reference number: A36475; MUID:91045991
 A:Accession: A36475
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195; 'R',197-461 <KOH>
 A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
 R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,
 Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular
 A:Reference number: A48416; MUID:91370690
 A:Accession: A48416
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-461 <DBM>
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AAI19824.1; PID:g235649
 A>Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)
 R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons
 A:Reference number: A36007; MUID:90349572
 A:Accession: A36007
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 116-140; 'P',142-195; 'R',197-362; 'T',364-461 <HEL>
 A:Cross-references: GB:M35857; NID:g339751; PIDN:AAI63362.1; PID:g339752
 R:Loetscher, H.; Schlaepper, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus,
 J. Biol. Chem. 265, 20131-20138, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor

Query Match	13.88;	Score 211.5;	DB 1;	Length 416;
Best Local Similarity	30.68;	Pred. No. 5.8e-07;		
Matches 77; Conservative	23;	Mismatches 101;	Indels 51;	Gaps 13;

```

C:Superfamily: tumor necrosis factor receptor type 1, NGF receptor repeat homology

Query Match          13.6%; Score 209.5; DB 2; Length 435;
Best Local Similarity 24.5%; Pred. No. 8.2e-07;
Matches 67; Conservative 27; Mismatches 87; Indels 93; Gaps 9;

OY 37 PSNDRCHECHPRGNGMVSRCRSRONTVCRCPCGPGFYNDVYSSK-CRPTCINLRSGSER 95
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 53 PQHRTACRCRCPGTYVSAKSKSRIDTYCATCAEWSYNHMYLYITCQLCRCRDYMKLEE 112
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 96 KOLCTATQDPTVCCRCAG-----TQPLDSYKPGVD-----CACP 130
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 113 IAPCTSKRKTQCRQCPGMFCAMALECTHCELLSDPCPGTEALKEDEVGKGNHHCVCCKA 172
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 131 GHF---SPDNDQACKWNTCTIAGKHTLQPAANSSDPAICEDDPATQOETQSGPARPIT 188
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 173 GHFQNTSSPSARCKQHTTCEENQGLVEAAPGTAQSDTTCN-----PLEPL- 217
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 189 VQPTAMPRTSQGPRTREVEYVGGRAVAAILGLVLGLPLAILLAL----- 237
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 218 -----PPEKSGTM-----LMLAVLLPLAFLLIATVFCISKSH 251
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 238 -----YLLRNDQRLPDAHKRPPGSGSFRTP 262
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 252 PSICKRLKSLTKRRPQGEPPN-----PVAGSWEP 281
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 10
A66476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A66476, A46515
J.Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of mur
A:Reference number: A46476; MUID:92105763
A:Accession: A66476
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: GB:M83312; NID:g1553058
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIPI:75207)
J.Rigimadal, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay
J. Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:93094586
A:Accession: A46515
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287, 'LV' <ORI>
A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
A:Experimental source: BALB/c, liver
A:Note: sequence extracted from NCBI backbone (NCBIPI:120357)
C:Comment: For an alternative splice form, see PIR:A46515.
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match          13.6%; Score 209; DB 2; Length 305;
Best Local Similarity 22.0%; Pred. No. 6.5e-07;
Matches 64; Conservative 39; Mismatches 96; Indels 92; Gaps 9;

OY 26 VTGLH-----CYGDPTYSNDRCHCHPRGNGMVSRCRSRONTVCRCPCGPGFYNDVYSSK 79
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 15 LTAHVLGOCVTCSDKQYIHDGQCDLCPGSRILTSHCTALEKTQCHPCDSEGSFAQNNRE 74
      + : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
OY 80 -PCKCTCNCNLRSGSERCOLCTATQDPTVCCRCAG----- 112

```


Wed Jun 19 05:54:53 2002

us-09-852-845-2.rpr

Page 8

Db 246 IICRDSAP-VKEVEGESITVTKPLTPASIPFSSNPFENPTLGFSTTPRESHPVSSPTIS 303

Qy 209 -----VPGRAVAATLGLG-LVTLGLGPLAI 233

Db 304 PVEGRSNMHNFPVPRVEVVPYQGDPRLLYGLSLNVPRI 340

Search completed: June 18, 2002, 14:24:43
Job time: 46 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:24:46 ; Search time 11.65 Seconds

(Without alignments)
920.628 Million cell updates/sec

Title: US-09-852-845-2
Perfect score: 1538
Sequence: 1 MCVGARLRGRCPCALLLLG.....SFRTPIQEPOADHSTLAKI 277

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
1	1538	100.0	277 1	TNR4_HUMAN
2	864.5	56.2	271 1	TNR4_RAT
3	857	55.7	272 1	TNR4_MOUSE
4	248.5	16.2	415 1	TNR3_MOUSE
5	247	16.1	616 1	TR11_HUMAN
6	224.5	14.6	427 1	TR16_HUMAN
7	221.5	14.4	277 1	TNR5_HUMAN
8	221.5	14.4	625 1	TR11_MOUSE
9	217	14.1	461 1	TR1B_HUMAN
10	216	14.0	425 1	TR16_RAT
11	211.5	13.8	416 1	TR16_CHICK
12	209.5	13.6	435 1	TNR3_HUMAN
13	209	13.6	289 1	TNR5_MOUSE
14	202.5	13.2	256 1	TNR9_MOUSE
15	202.5	13.2	474 1	TR1B_MOUSE
16	194.5	12.6	283 1	TR1A_HUMAN
17	187.5	12.2	269 1	TNR5_BOVIN
18	186.5	12.1	255 1	TNR9_HUMAN
19	172	11.2	461 1	TR1A_RAT
20	171	11.1	327 1	TNR6_MOUSE
21	166.5	10.8	259 1	T10C_HUMAN
22	162	10.5	241 1	TR18_HUMAN
23	161	10.5	454 1	TR1A_MOUSE
24	160.5	10.4	325 1	VR2_SFVLA
25	152	9.9	326 1	VR2_MYXVL
26	147.5	9.6	324 1	TNR6_RAT
27	147	9.6	595 1	TNR8_HUMAN
28	146.5	9.5	349 1	VC22_VARY
29	145.5	9.4	3110 1	LM42_HUMAN
30	144.5	9.4	260 1	TNR7_HUMAN
31	144.5	9.4	323 1	TNR6_BOVIN
32	144.5	9.4	1581 1	LMG3_MOUSE
33	144	9.4	461 1	TR1A_PIG

34	142	9.2	250 1	TNR7_MOUSE	P41272 mus musculus
35	140	9.1	471 1	TR1A_BOVIN	O19131 bos taurus
36	139	9.0	1587 1	LMG3_HUMAN	O9Y6N6 homo sapien
37	139	9.0	3075 1	LM41_HUMAN	P25391 homo sapien
38	138	9.0	1798 1	LMB2_HUMAN	P35268 homo sapien
39	134	8.7	417 1	TR12_HUMAN	O93038 h wsl-1 pro
40	132	8.6	1801 1	LMB2_RAT	P15800 rattus norv
41	131.5	8.6	332 1	TNR6_PIG	O77736 sus scrofa
42	129.5	8.4	440 1	T10B_HUMAN	O14763 homo sapien
43	129	8.4	1696 1	PK5_BRACL	O9J115 branchiosto
44	128.5	8.4	1713 1	LM43_HUMAN	O16787 homo sapien
45	128	8.3	3718 1	LM45_MOUSE	O61001 mus musculus

ALIGNMENTS

```

RESULT 1
ID      TNR4_HUMAN
AC      P43489; 013663;
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DE      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE      receptor) (ACT35 antigen) (TAX-transcriptionally activated
DE      glycoprotein 1 receptor) (CD134 antigen).
GN      TNFRSF4 OR TNXP1L.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_Taxid=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94170844; PubMed=7510240;
RA      Latza U., Duerkop H., Schmittiger S., Ringeling J., Eitelbach F.,
RA      Hummel M., Fonatsch C., Stein H.;
RT      "The human OX40 homolg: cDNA structure, expression and chromosomal
RT      assignment of the ACT35 antigen.";
RL      Eur. J. Immunol. 24:677-683(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95219871; PubMed=7704935;
RA      Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA      Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT      "Identification of OX40 ligand and preliminary characterization of
RT      its activation on OX40 receptor.";
RL      Cite. Shock 44:30-34(1994).
CC      - FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC      - SUBCELLULAR LOCATION: Type I membrane protein.
CC      - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC      - DATABASE: NAME=PROT; NOTE=CD guide CD134 entry;
CC      NAME="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: X75962; CAA53576.1; -.
DR      EMBL: S76792; AAB33944.1; ALT_INT.
DR      HSRP: P25942; ICDP.
DR      MIM: 600315; -.
DR      InterPro: IPR001368; TNFR_c6.
DR      Pfam: PF00020; TNFR_c6; 3.
DR      ProDom: PD000771; TNFR_c6; 1.
DR      SMART: SM00208; TNFR: 3.
DR      PROSITE: PS00652; TNFR_NGFR_1; 3.
DR      PROSITE: PS50050; TNFR_NGFR_2; 2.
DR      Receptor: T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW

```

KM Signal. 1 28 POTENTIAL.
 FT SIGNAL 29 277 TUMOR NECROSIS FACTOR RECEPTOR
 FT CHAIN 29 277 SUPERFAMILY MEMBER 4.
 FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 215 235 POTENTIAL.
 FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 30 65 TNFR-CYS 1.
 FT REPEAT 66 107 TNFR-CYS 2.
 FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).
 FT REPEAT 127 167 TNFR-CYS 4.
 FT CAROHD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CAROHD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 277 AA; 29340 MM; 49F13523941350BF CRC64;

Query Match 100.0%; Score 1538; DB 1; Length 277;
 Best Local Similarity 100.0%; Pred. No. 4, 1e-99;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVGARRLGRPCALLLLGLSTVGLHCYDTPPSNDRCHCRPGNGMVSRSRQ 60
 DB 1 MCVGARRLGRPCALLLLGLSTVGLHCYDTPPSNDRCHCRPGNGMVSRSRQ 60
 QY 61 NTVCRCGCGFYNDVSSSRCKPCCTWCNLRSGSERKQLCTATQDYCRCRAGTQPLDSYK 120
 DB 61 NTVCRCGCGFYNDVSSSRCKPCCTWCNLRSGSERKQLCTATQDYCRCRAGTQPLDSYK 120
 QY 121 PGVDCAFCPGHSPGDNDACKPMTNCTLAGKHTLQPASSNSDAICEDBDPPATQPEHQ 180
 DB 121 PGVDCAFCPGHSPGDNDACKPMTNCTLAGKHTLQPASSNSDAICEDBDPPATQPEHQ 180
 QY 181 GPAPRITVQPTLEAMPRISQGPSTRPEVEVGGRAVAAILGLGLVGLLPLAILLALYLL 240
 DB 181 GPAPRITVQPTLEAMPRISQGPSTRPEVEVGGRAVAAILGLGLVGLLPLAILLALYLL 240
 QY 241 RRDORLPDAHKKPGGGSFRTPIOEODAHSTLAKI 277
 DB 241 RRDORLPDAHKKPGGGSFRTPIOEODAHSTLAKI 277

RESULT 2
 TNRA_RAT
 ID TNRA_RAT STANDARD; PRT: 271 AA.
 AC P15725;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen) (MRC OX40).
 GN TNFRSF4 OR TXGPIL OR OX40.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID-10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-T-cell;
 RX MEDLINE-90214614; PubMed-2157591;
 RA Mallett S., Fossum S., Barclay A.N.;
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";
 RL EMBO J. 9:1063-1068(1990).
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - CC the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X17037; CAA34897.1; .
 DR PIR: S08036; S08036.
 DR PIR: S12783; S12783.
 DR HSSP: P19438; 1EXT.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 3.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR.1; 3.
 DR PROSITE: PS00650; TNFR_NGFR.2; 2.
 DR PROSITE: T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
 KW Signal.
 FT SIGNAL 1 19 POTENTIAL.
 FT CHAIN 20 271 TUMOR NECROSIS FACTOR RECEPTOR
 FT TRANSMEM 211 235 SUPERFAMILY MEMBER 4.
 FT DOMAIN 236 271 EXTRACELLULAR (POTENTIAL).
 FT REPEAT 25 60 POTENTIAL.
 FT REPEAT 61 102 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 103 123 TNFR-CYS 1.
 FT REPEAT 124 164 TNFR-CYS 2.
 FT CAROHD 143 143 TNFR-CYS 3 (INCOMPLETE).
 FT CAROHD 143 143 TNFR-CYS 4.
 SQ SEQUENCE 271 AA; 29895 MM; C06465136B16E821 CRC64;

Query Match 56.2%; Score 864.5; DB 1; Length 271;
 Best Local Similarity 63.4%; Pred. No. 6, 5e-53;
 Matches 168; Conservative 18; Mismatches 74; Indels 5; Gaps 3;

QY 15 ALLLLGLSTVGLHCYDTPPSNDRCHCRPGNGMVSRSRONTVCRCGPGFYND 74
 DB 10 AFLLLGLSLGVTVKLCNCVADTPVSGHKCCREGCPGNGMVSRCRHTBDYCHPCPEGFYNE 69
 QY 75 VVSKRCRCCTCNLRSGSERKQLCTATQDYCRCRAGTQPL--DSYKGVCAAPCPGH 132
 DB 70 AVNYDCKQCTQCNHRSGSELKQCTPTEDYVCQCRPGTQPRODSSHKLGVDVCPGPH 129
 QY 133 FSPGDNDACKPMTNCTLAGKHTLQPASSNSDAICEDBDPPATQPEHQPPARITVQPT 192
 DB 130 FSPGSDNDACKPMTNCTLAGKHTLQPASSNSDAICEDBDPPATQPEHQPPARITVQPT 189
 QY 193 EAMPRISQGPSTRPEVEVGGRAVAAILGLGLVGLLPLAILLALYLLRRDORLPDAH 252
 DB 190 TVMPRTSQPSPTLVAPGPAFAVILGLG--LGLLPLVLLALYLLRKAMR--SPNTPK 246
 QY 253 PGGGSFRTPIOEODAHSTLAKI 277
 DB 247 PCWGNSEFRTPIOEODAHSTLAKI 271

RESULT 3
 TNRA_MOUSE
 ID TNRA_MOUSE STANDARD; PRT: 272 AA.
 AC P47741;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen).
 GN TNFRSF4 OR TXGP1 OR OX40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID-10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C;
 RX MEDLINE-94044750; PubMed-8228223;
 RA Calderhead D.M., Buhlmann J.E., van den Bertwegh A.J.,

RA Claassen E., Noelle R.J., Fell H.;
 RT "Cloning of mouse OX40: a T cell activation marker that may mediate
 RT T-B cell interactions.";
 RL J. Immunol. 151:5261-5271(1993).
 RN [2].
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95255413; PubMed=7737295;
 RA Birkehead M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,
 RA Barclay A.N.;
 RT "Gene structure and chromosomal localization of the mouse homologue
 RT of rat OX40 protein.";
 RL Eur. J. Immunol. 25:926-930(1995).
 CC - FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: Z21674; CAAT9772.1; -;
 CC EMBL: X85214; CA59476.1; -;
 CC HSSP: P19438; IEXT.
 CC MGD: MGI:104512; Tnfisf4.
 CC InterPro: IPR001368; TNFR_c6.
 CC Pfam: PF00020; TNFR_c6; 3.
 CC ProDom: PD000771; TNFR_c6; 1.
 CC SMART: SM00208; TNFR; 3.
 CC PROSITE: PS00652; TNFR_NGFR_1; 3.
 CC PROSITE: PS50050; TNFR_NGFR_2; 2.
 CC KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
 KW Signal.
 FT SIGNAL. 1 19 POTENTIAL.
 FT CHAIN 20 272 TUMOR NECROSIS FACTOR RECEPTOR
 FT TRANSMEM 20 272 SUPERFAMILY MEMBER 4.
 FT DOMAIN 20 216 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 212 236 POTENTIAL.
 FT REPEAT 237 272 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 26 61 TNFR-CYS 1.
 FT REPEAT 62 103 TNFR-CYS 2.
 FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).
 FT REPEAT 125 165 TNFR-CYS 4.
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CONFLICT 15 15 A -> G (IN REF. 2).
 SQ SEQUENCE 272 AA; 30153 MW; 06E7BA156F0D08E CRC64;
 Query Match 55.7%; Score 857; DB 1; Length 272;
 Best Local Similarity 63.5%; Pred. No. 2,1e-52;
 Matches 169; Conservative 20; Mismatches 71; Indels 6; Gaps 4;

Db 247 KPCWGNSEFRPTIOEHTDAHFTLAKI 272
 RESULT 4
 ID TNFR_MOUSE STANDARD; PRT; 415 AA.
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Lymphotoxin-beta receptor precursor.
 GN LYBR OR TNFRSF3.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RX MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression.";
 RL J. Immunol. 155:5280-5288(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping.";
 RL Genomics 30:312-319(1995).
 CC - FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
 CC IMMUNE DEVELOPMENT.
 CC - SUBCELLULAR LOCATION: Type I membrane protein.
 CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U29173; AAA6864.1; -;
 CC EMBL: U38423; AAB00846.1; -;
 CC EMBL: U30798; AAB1334.1; -;
 CC HSSP: P25942; ICDP.
 CC MGD: MGI:104875; Ltbr.
 CC InterPro: IPR001368; TNFR_c6.
 CC Pfam: PF00020; TNFR_c6; 3.
 CC ProDom: PD000771; TNFR_c6; 1.
 CC SMART: SM00208; TNFR; 3.
 CC PROSITE: PS00652; TNFR_NGFR_1; 2.
 CC PROSITE: PS50050; TNFR_NGFR_2; 3.
 CC KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL. 1 30 POTENTIAL.
 FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.
 FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 224 244 POTENTIAL.
 FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 42 81 TNFR-CYS 1.
 FT REPEAT 82 124 TNFR-CYS 2.
 FT REPEAT 125 170 TNFR-CYS 3.
 FT REPEAT 171 213 TNFR-CYS 4.
 FT DISULFD 43 58 BY SIMILARITY.
 FT DISULFD 59 72 BY SIMILARITY.
 FT DISULFD 62 80 BY SIMILARITY.
 FT DISULFD 83 98 BY SIMILARITY.
 FT DISULFD 101 116 BY SIMILARITY.
 FT DISULFD 104 124 BY SIMILARITY.

FT	DISULFID	126	132	BY SIMILARITY.
FT <th>DISULFID</th> <td>139</td> <td>150</td> <td>BY SIMILARITY.</td>	DISULFID	139	150	BY SIMILARITY.
FT <th>DISULFID</th> <td>142</td> <td>169</td> <td>BY SIMILARITY.</td>	DISULFID	142	169	BY SIMILARITY.
FT <th>DISULFID</th> <td>172</td> <td>187</td> <td>BY SIMILARITY.</td>	DISULFID	172	187	BY SIMILARITY.
FT <th>CARBOHYD</th> <td>40</td> <td>40</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	40	40	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>CARBOHYD</th> <td>179</td> <td>179</td> <td>N-LINKED (GLCNAC. . .) (POTENTIAL).</td>	CARBOHYD	179	179	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT <th>SEQUENCE</th> <td>415 AA;</td> <td>44956 MW;</td> <td>299326A566AEF661 CRC64;</td>	SEQUENCE	415 AA;	44956 MW;	299326A566AEF661 CRC64;
Query Match		16.2%;	Score 248.5;	DB 1; Length 415;
Best Local Similarity		23.3%;	Pred. No. 1.7e-10;	
Matches	93;	Conservative	39;	Mismatches 126; Indels 141; Gaps 16;
QY	7 RLGR--GFCAL--LLGLGLSTVYTGILHCVGDTY-----	-PSNRCHE	45	
DB	2 RLPRASSPCGLAMGFLLLGLSLGLVAASQQLVPRYRIENQTCMDQKEXYERIMHIVCSGR	61		
QY	46 CRRGGMWVSRCSRONTVCRRPCGPGFYNDVVS-KRCSTCMNLRSGERKOLATAD	104		
DB	62 CRRGFEVAVCSRSDTYCKTCRPHNSYNHNMHLSTQLCRCRDIVLGFEEVAPCSDBRK	121		
QY	105 TYCRRAG-----TOPLDSTKPG-----	VDCARCPGHP--SP	135	
DB	122 AECRCQPGKSCYLLDNECHCEERVLVLCQPTGEAEVDEIMDTVNCVPCRGHQNIS	181		
QY	136 GDNQACKRPWTNLGKHTLPLAPSSSDAICEDRPPAT-----		174	
DB	182 SPRACQPHTRCEIOGLVEAAGTSYSDTICKNPEPGAMLLALILSLVLEFLTTVLA	241		
QY	175 -----QPEOTGPP-----	ARRI-----	TYQPTFAWPR	197
DB	242 CAMMHNPISLCRLGLTLKRHPGEGSPRCRAPRADHPFDLAPLPMGSLSPSPAGRP	301		
QY	198 TS-----QGSTREPV--PGRAVAALIGLG-VLGLGRLAILALYLRL--	241		
DB	302 TAPSLSEEVVLAQOSPLVQARLEAERBEHGVAHGANGIHVNG--GSVTVTGNIYIYNGP	359		
QY	242 -----RDQRLPPDAHKP-----	PGGGSRTPTQEE	266	
DB	360 VLGTRGPGDPPAPPEPPYPRPEEGAPSESLTPYQED	398		
RESULT	5			
TR11_HUMAN				
ID	TR11_HUMAN	STANDARD:	PRT:	616 AA.
AC	Q9Y606;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 11A precursor			
DE	(Receptor activator of NF-kB) (Osteoclast differentiation factor			
DE	receptor) (OOPR).			
GN	TNFRSF11A OR RANK.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euteria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Dendritic cell;			
RC	MEDLINE=98032977; PubMed=9367155;			
RA	Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,			
RA	Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,			
RA	Galibert L.;			
RT	"A homologue of the TNF receptor and its ligand enhance T-cell growth			
RT	and dendritic-cell function.";			
RL	Nature 390:175-179(1997).			
RN	[2]			
RP	FUNCTION.			
RX	MEDLINE=99097247; PubMed=9878548;			
RA	Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,			
RA	Motomida T., Higashio K.;			
RT	"RANK is the essential signaling receptor for osteoclast			

RN	[3]	differentiation factor in osteoclastogenesis".
RL	Biochem. Biophys. Res. Commun.	253:395-400(1998).
RP	VARIANT FEO 16-L-L-21 DUPL, VARIANT PDB2 13-A--L-21 DUPL, AND VARIANT V-192.	
RX	MEDLINE=20082806; PubMed=10615125;	
RA	Hughes A.E., Ralston S.H., Marken J., Bell C., Macpherson H., Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hoyv L., Anderson D.M.,	
RA	"mutations in TNFRSF11A, affecting the signal peptide of RANK, cause familial expansile osteolysis."	
RL	Nat. Genet.	24:45-48(2000).
CC	-I- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL), ALSO KNOWN AS OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.	
CC	-I- SUBCELLULAR LOCATION: Type I membrane protein (Potential).	
CC	-I- TISSUE SPECIFICITY: Ubiquitous expression with high levels in skeletal muscle, thymus, liver, colon, small intestine and adrenal gland.	
CC	-I- DISEASE: DEFECTS IN TNFRSF11A ARE THE CAUSE OF FAMILIAL EXPANSILE OSTEOLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELING. THE OSTEOCLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING EARLY ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS AND LOSS OF DENTITION.	
CC	-I- DISEASE: DEFECTS IN TNFRSF11A ARE A CAUSE OF FAMILIAL PAGET DISEASE OF BONE, ALSO KNOWN AS PAGET DISEASE OF BONE 2 (PDB2). IT IS A BONE REMODELLING DISORDER WITH CLINICAL SIMILARITIES TO FEO. UNLIKE FEO, HOWEVER, AFFECTED INDIVIDUALS HAVE INVOLVEMENT OF THE AXIAL SKELETON WITH LESIONS IN THE SPINE, PELVIS AND SKULL.	
CC	-I- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.	
CC	-----	
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isdb-sib.ch/announce/or send an email to license@isb.sib.ch).	
CC	EMBL; AF018253; AAB86809.1; -	
DR	HSP; P25942; ICDF.	
DR	MIM; 603499; -	
DR	MIM; 174810; -	
DR	MIM; 602080; -	
DR	InterPro; IPRO01368; TNFR_C6.	
DR	Pfam; PF00020; TNFR_C6; 4.	
DR	ProDom; PD000771; TNFR_C6; 1.	
DR	SMART; SMO0208; TNFR; 4.	
DR	PROSITE; PS00652; TNFR_NGFR_1; 1.	
DR	PROSITE; PS50050; TNFR_NGFR_2; 1.	
KW	Receptor; Glycoprotein; Transmembrane; Repeat; Signal; Polymorphism; Disease mutation.	
FT	SIGNAL	1 .. 29
FT	CHAIN	30 .. 616
FT	DOMAIN TRANSKEM	213 .. 232
FT	DOMAIN	234 .. 616
FT	REPEAT	68 .. 68
FT	REPEAT	71 .. 112
FT	REPEAT	114 .. 151
FT	REPEAT	154 .. 194
FT	DISULFD	34 .. 46
FT	DISULFD	47 .. 60
FT	DISULFD	50 .. 68
FT	DISULFD	71 .. 86
FT	DISULFD	92 .. 112
FT	DISULFD	114 .. 127
FT	DISULFD	133 .. 151
FT	CARBOHYD	105 .. 105
FT	CARBOHYD	174 .. 174
FT	POTENTIAL.	
FT	TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11A.	
FT	EXTRACELLULAR (POTENTIAL).	
FT	POTENTIAL.	
FT	CYTOPLASMIC (POTENTIAL).	
FT	TNFR-CYS 1.	
FT	TNFR-CYS 2.	
FT	TNFR-CYS 3.	
FT	TNFR-CYS 4.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	BY SIMILARITY.	
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	N-LINKED (GLCNAC. . .) (POTENTIAL).	

```
FT VARIANT 13 21 ALLLICALL -> ALLLICALLALLLICALL (IN
FT PDB2).
FT VARIANT 16 21 /FTID-VAR_011516.
FT VARIANT 192 192 LICALL -> LICALLALLLICALL (IN FEO).
FT VARIANT 192 192 /FTID-VAR_011517.
FT VARIANT 192 192 A -> V.
FT SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;

Query Match 16.1%; Score 247; DB 1; Length 616;
Best Local Similarity 33.3%; Pred. No. 3.1e-10;
Matches 70; Conservative 21; Mismatches 83; Indels 36; Gaps 10;

QY 1 MCVGARRLRGRCALALLL-----GLGLSTVTLGLHCVGDT-YPSNDRCHCRPGNGV 54
DQ 1 MAPARRR--RRPLFALLLICALLRLVALDIAPPTSEKHEHLGRCCNCEPEKYMSS 58
QY 55 RCSRSONTVCRPGCGPFYNDVYSSK-PCKPCTWCNL-----RSGSERKOLCTA-- 101
DQ 59 KCTTSDSVCLPCGPDDELDSMNEDKCLLHKYCDTGKALVAVAGNSTTFRRCACGTAGY 118
QY 102 --TODTVYCRGACGTQ-----PLDSYKPGVDCAPCPGHPSP--GDNOACKFWINCT 148
DQ 119 HWSQDCEC-CHRNTECAFGALGAOHPLQLNKDTV--CKPLAGYFSDAFSTDKCRFWINCT 176
QY 149 LAGKHTLQPASNSDAICEDRDPRATOPQE 178
DQ 177 FLGKRVEHGHTEKSDAVCSSLPARKPPNE 206

RESULT 6
TR16_HUMAN ID TR16_HUMAN STANDARD; PRT; 427 AA.
AC P08138;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE affinity nerve growth factor receptor) (NGF receptor) (p580-LINGR)
DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN NGFR OR TNFRSF16.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87051725; PubMed=3022937;
RA Johnson D., Lananhan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
RA Bothwell M., Chao M.;
RT "Expression and structure of the human NGF receptor.";
RL Cell 47:545-554(1986).
RN [2]
RP SEQUENCE OF 1-22 FROM N.A.
RX MEDLINE=89096903; PubMed=2850481;
RA Sehgal A., Patil N., Chao M.;
RT "A constitutive promoter directs expression of the nerve growth factor
RT receptor gene.";
RL Mol. Cell. Biol. 8:3160-3167(1988).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,
CC AND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF
CC NEURAL CELLS.
CC -1- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
CC INTERACTS WITH P75NTR-ASSOCIATED CELL DEATH EXECUTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
```

```
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M14764; AAB59544.1; -
DR EMBL; M21621; AAA36363.1; -
DR PIR; A25218; GOHUN.
DR HSSP; P07174; INGR.
DR MIM; 162010; -
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00531; death.1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 3.
DR PROSITE; PS50050; TNFR_NGFR_2; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW Phosphorylation; Signal; Apoptosis.
FT SIGNAL 1
FT CHAIN 29
FT DOMAIN 29 427
FT TRANSMEM 251 272
FT DOMAIN 273 427
FT REPEAT 31 64
FT REPEAT 66 107
FT REPEAT 108 146
FT REPEAT 148 188
FT DOMAIN 344 421
FT DOMAIN 197 248
FT DISULFID 32 43
FT DISULFID 44 57
FT DISULFID 47 64
FT DISULFID 67 83
FT DISULFID 86 99
FT DISULFID 89 107
FT DISULFID 109 122
FT DISULFID 125 138
FT DISULFID 128 146
FT DISULFID 149 164
FT DISULFID 167 180
FT DISULFID 170 188
FT CARBOHD 60
FT SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64;

Query Match 14.6%; Score 224.5; DB 1; Length 427;
Best Local Similarity 30.1%; Pred. No. 7.9e-09;
Matches 84; Conservative 31; Mismatches 95; Indels 69; Gaps 16;

QY 3 VGARRLRG--GP-CALLLLGLGL-----STVTGLHCVGDTYPSNDRCHCRPGNGV 53
DQ 1 MGAGATGRAMGPRLLLLLLGLVSLGAKKACPTGL-----YTHSGECKKCNLGEVYA 54
QY 54 SFRCSQNTVCRPGCGPF-YNDVYS-SKPKCKCTWC-NLRSGSERKOLCTATQTVYCR-- 108
DQ 55 QPCGANQ-TVCEPCIDSVTFSDVVSATBCKCTCEVGLQMSAP---CVEADDAVCRQA 110
QY 109 -----CRAGTQPLDSY--KPGVCAAPCPGHPSPGDNQA--CKPWTNC 147
DQ 111 YGYVDENTTGRCACRVCEAGSGLVFSCODKONTVCCECPDGTYSDEAHNVDPCLPCTYC 170
QY 148 TLGKHTLQPASNSDAICED-----RDPPATOPQETGPPRPATVYOPTE 193
DQ 171 E-DTRQLRECTRMADABCEELIPGRWITRSTPEGSDSTAPSTQPEAPPEQDL-IASIV 228
QY 194 AMPRTSQGPSTPVE-----VPGRAVVAAILGLGLV 224
DQ 229 AGVTVTMGSSQPVYRTGTTNMLIPVYCSIIAAVVVGLV 267
```

RESULT	7			
ID	TNR5_HUMAN	STANDARD:	PRT:	277 AA.
AC	P25942;			
DT	01-MAY-1992 (Rel. 22, Created)			
DT	01-MAY-1992 (Rel. 22, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 5 precursor (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CDw40).			
CN	TNR55 OR CD40.			
OS	Human sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxId:9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE:89356608; PubMed:2475341;			
RA	Stamenkovic I., Clark E.A., Seed B.;			
RT	"A B-lymphocyte activation molecule related to the nerve growth factor receptor and induced by cytokines in carcinomas."			
RL	EMBO J. 8:1403-1410(1989).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	DeLours P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,			
RA	Jones M., Stavrvides G., Almeida J.P., Babbage A.K., Baggaley C.L.,			
RA	Ballay J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,			
RA	Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,			
RA	Buck D., Burrill W., Butler A.P., Carter C., Carter N.P.,			
RA	Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,			
RA	Clegg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,			
RA	Colson A.G., Coville G.J., Deaman R., Dhani P., Dunn M.,			
RA	Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,			
RA	Grafham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,			
RA	Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,			
RA	Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,			
RA	Kay M.P., Kimberley A.M., King A., Knigths A., Laird G.K., Lawlor S.,			
RA	Lehvasalo M.H., Leverisa M., Lloyd C., Lloyd D.M., Lovell J.D.,			
RA	Marsh V.L., Martin S.L., McConachie L.J., McLeay K., Murray A.A.,			
RA	Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,			
RA	Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,			
RA	Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,			
RA	Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,			
RA	Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,			
RA	Sween M., Sycamores N., Taylor R., Tee L., Thomas D.W., Thorpe A.,			
RA	Tracey A., Tromens A.C., Vaudin M., Wall M., Wallis J.M.,			
RA	Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,			
RA	Wilmink L., Wray P.W., Hubbard T., Durdin R.M., Bentley D.R., Beck S.,			
RA	Rogers J.;			
RT	"The DNA sequence and comparative analysis of human chromosome 20."			
RL	Nature 414:865-871(2001).			
RN	[3]			
RP	3D-STRUCTURE MODELING OF 24-144.			
RX	MEDLINE:97189482; PubMed:9037712;			
RA	Bajorath J., Aurilio A.;			
RT	"Construction and analysis of a detailed three-dimensional model of the ligand binding domain of the human B cell receptor CD40."			
RL	Proteins 27:59-70(1997).			
RN	[4]			
RP	3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.			
RX	MEDLINE:98266353; PubMed:9605317;			
RA	Slingsh J., Garber E., van Viljmen H., Karpusas M., Hsu Y.-M.,			
RA	Zheng Z., Natsmith J.H., Thomas D.;			
RT	"The role of polar interactions in the molecular recognition of CD40L with its receptor CD40."			
RL	Protein Sci. 7:1124-1135(1998).			
CC	-1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.			
CC	-1- SUBCELLULAR LOCATION: TYPE I membrane protein.			
CC	-1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.			
CC	-1- SIMILARITY: CONTAINS 4 TNR5-CYS REPEATS.			
CC	-1- DATABASE: NAME=PROT; NOTE=CD guide CD40 entry;			
CC	WWW=http://www.ncbi.nlm.nih.gov/Proteome/cd/cd40.htm"			

	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation at the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/isb-ch).
DR	EMBL; X60592; CAA43045.1;	-
DR	EMBL; AL035662; CAC17670.1;	-
DR	PIR; S04460; S04460.	
DR	PDB; ICDF; 01-APR-97.	
DR	MIM; 109535;	
DR	InterPro; IPR001368; TNFR_c6.	
DR	Pfam; PF00020; TNFR_c6; 4.	
DR	Prodom; PD000771; TNFR_c6; 1.	
DR	SMART; SM00208; TNFR; 4.	
DR	PROSITE; PS00652; TNFR_NGR_1; 1.	
DR	PROSITE; PS50050; TNFR_NGR_2; 4.	
KW	Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal; 3D-structure.	
KW	3D-structure.	
FT	SIGNAL	1 19 POTENTIAL.
FT	CHAIN	20 277 TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 5 EXTRACELLULAR (POTENTIAL).
FT	DONAIN	20 193 TRANSMEM
FT	TRANSSEM	194 215
FT	DOMAIN	216 277 CYTOPLASMIC (POTENTIAL).
FT	REPEAT	25 60 TNFR-CYS 1.
FT	REPEAT	61 103 TNFR-CYS 2.
FT	REPEAT	104 144 TNFR-CYS 3.
FT	REPEAT	145 187 TNFR-CYS 4.
FT	DISULFID	26 37
FT	DISULFID	38 51
FT	DISULFID	41 59
FT	DISULFID	62 77
FT	DISULFID	83 103
FT	DISULFID	105 119
FT	DISULFID	111 116
FT	DISULFID	125 143
FT	CARBOHYD	153 153
FT	CARBOHYD	180 180
SO	SEQUENCE	277 AA; 30619 MW; BC8776EC2CA5680 CRC64;
OY	Query Match	14.4%; Score 221.5; DB 1; Length 277;
BEST	Local Similarity	23.2%; Pred. No. 8.7e+09;
Match	66; Conservative	34; Mismatches 95; Indels 89; Gaps 10.
OY	26 VTGLH-----CVGDYTSNDRCHCECRGNGMVRCSRQNTVCRCPCGGFYNDVSSK	79
Db	15 LTAVHPPEPTACREKOYLINSQCCLSGQGLYVDCTFEFTBELPCGESEFLDTWNRE	74
OY	80 P-CRKETWCNLRSGERKQLCTATODTVLCRCRAGTOPLD-----SYKPYVD---	124
Db	75 THCHOHKKCDDPLGLAYVOOKGTSETDTICTCEEHNCTSEACECVLIHRSCSPGVKQI	134
OY	125 -----CARPRPHFSRGDN--CACKRYMTCTLAGKHTLTLPANSSPAICEDDPRAIT	174
Db	135 ATGVSDTICEPRVGFESNVSAFEKCPHWISCEPKDKLVDOAGTKTDVV-----	186
OY	175 QPOETQGPPAREITVQPTTEAMPTSOGSTREVEYVGGRFAVAAILGLVLTLPLPALIL	234
Db	187 -----GPQDR-----LVALVIPILFIIGIL--FAII	209
OY	235 LALYLRLRDQRLP---PDANKRP-----GGGSFTPTIOE	265
Db	210 LVLFVKIKVAKKPKNKAPRKHQEPQEIINFDDLPGSNTAFAVOE	253
RESULT	8	
ID	TRIL_MOUSE	
ID	TRIL_MOUSE	
NC	035305;	
	STANDARD:	PRT; 625 AA.

DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 11A precursor
 DE (receptor activator of NF-kB) (osteoclast differentiation factor
 DE receptor) (ODFR).
 GN TNFRSF11A OR RANK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Fetal liver;
 RX MEDLINE=98032977; PubMed=9367155;
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 RN [2]
 RP FUNCTION
 RX MEDLINE=99097247; PubMed=9878548;
 RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
 RA Morinaga T., Higashio K.;
 RT "RANK is the essential signaling receptor for osteoclast
 RT differentiation factor in osteoclastogenesis.";
 RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
 CC -1- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL). ALSO KNOWN AS
 CC OSTEOCLAST DIFFERENTIATION FACTOR OR ODF). ESSENTIAL FOR RANKL-
 CC MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
 CC INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
 CC -1- TISSUE SPECIFICITY: UBQUITOUS EXPRESSION WITH HIGH LEVELS IN
 CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
 CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: AF019046; AAB86810.1; -;
 DR HSSP: P25942; ICDF.
 DR MGD: MGI:1314891; Tnf1rsf11a.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF000020; TNFR_c6; 3.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 KM Receptor: Glycoprotein; Transmembrane: Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 1 625
 FT 1 625
 FT DOMAIN 31 214
 FT TRANSMEM 235 234
 FT DOMAIN 215 625
 FT REPEAT 35 69
 FT REPEAT 72 113
 FT REPEAT 115 152
 FT REPEAT 155 195
 FT DISULFID 35 47
 FT DISULFID 48 61
 FT DISULFID 51 69
 FT DISULFID 72 87
 FT DISULFID 93 113
 FT DISULFID 115 128

FT DISULFID 134 152 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SO SEQUENCE 625 AA; 66621 MW; F8C1872E95911DBE CRC64;
 Query Match 14.4%; Score 221.5; DB 1; Length 625;
 Best Local Similarity 30.3%; Pred. No. 1.8e-08;
 Matches 67; Conservative 17; Mismatches 84; Indels 53; Gaps 10;
 Oy 1 MCVGARRLRGPCAAAL----LLLGISTVYGLHCVDPT-YPSNDRCCHECPNGMYSR 55
 Db 1 MAPRARRRRLPAPLALCVLLVPLQVTLQVTPPTOERHYEHLRCCSRCEPGKYLSSK 60
 Oy 56 CSRSNTWCRCPCGPGFYNDVVSRSKRCRCCTM-----CNLRS-----GSE 94
 Db 61 CTPSDSVCLPCGPDVEYLD-----TWNEEDKCLHKYCDAGKALVAADPGNHTAP 110
 Oy 95 RKOLCTA----TQDVCRCRAGTQ-----PLDSYKPGVDCAPCPGHFSP--GDNQ 139
 Db 111 RRCACTAGYHWNNSDCEC-CRRNTECAPGFGAHPQLKNDIV-CIPCLLGFPSDFVSSTD 168
 Oy 140 ACKPWTNCTLAGKHTLPASNSSDAICEDRDPPATQPEETQ 180
 Db 169 KCKPWTNCTLLGKLEAHOGTTESDYVCCSSMTLRPPREAQ 209
 RESULT 9
 TRIB_HUMAN STANDARD; PRT; 461 AA.
 ID TRIB_HUMAN
 AC P20333;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor
 DE binding protein 2) (TBPI) (p80) (TNF-R2) (p75) (CD120b) (Ectanecept).
 GN TNFRSF1B OR TNFR2 OR TNFR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90260639; PubMed=2160731;
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,
 RA Dower S.K., Cosman D., Goodwin R.G.;
 RT "A receptor for tumor necrosis factor defines an unusual family of
 RT cellular and viral proteins.";
 RL Science 248:1019-1023(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91045991; PubMed=2172983;
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;
 RT "A second tumor necrosis factor receptor gene product can shed a
 RT naturally occurring tumor necrosis factor inhibitor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96299745; PubMed=8661109;
 RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,
 RA Lepeslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;
 RT Broder G.M.;
 RL "Physical mapping and genomic structure of the human TNFR2 gene.";
 RN Genomics 35:94-100(1996).
 RN [4]
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=90349572; PubMed=2166946;
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,
 RA Ringold G.M.;
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor
 RT and demonstration of a shed form of the receptor.";
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).

[5]
 RN SEQUENCE OF 27-31.
 RP MEDLINE-90110215; PubMed-2153136;
 RA Engelmann H., Novick D., Wallach D.;
 RT "Two tumor necrosis factor-binding proteins purified from human
 RT urine. Evidence for immunological cross-reactivity with cell surface
 RT tumor necrosis factor receptors";
 RL J. Biol. Chem. 265:1531-1536(1990).
 RN [6]
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.
 RX MEDLINE-91056048; PubMed-2173696;
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.;
 RT "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from HL60 cells.";
 RL J. Biol. Chem. 265:20131-20138(1990).
 RN [7]
 RP CHARACTERIZATION.
 RX MEDLINE-93016040; PubMed-1328224;
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.;
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation";
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [8]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH
 RP TRAF2.
 RX MEDLINE-99221490; PubMed-10206649;
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Mu H.;
 RT "Structural basis for self-association and receptor recognition of
 RT human TRAF2";
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -1- PHARMACEUTICAL: Available under the name Embrel (Immunex and
 CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid
 CC arthritis (RA). Embrel consist of the extracellular ligand-binding
 CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to
 CC TNF-alpha and blocks its interactions with receptors.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;
 CC WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd120b.htm".
 CC -1- DATABASE: NAME-Embrel; NOTE-Clinical information on Embrel;
 CC WWW-"http://www.embrelinfo.com/".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-slb.ch/announce/
 CC or send an email to license@isb-slb.ch).
 CC -----
 DR EMBL: M32315; AAAS9929.1; -;
 DR EMBL: M35857; AAA63262.1; -;
 DR EMBL: U52165; AAC50622.1; JOINED.
 DR EMBL: U52156; AAC50622.1; JOINED.
 DR EMBL: U52157; AAC50622.1; JOINED.
 DR EMBL: U52158; AAC50622.1; JOINED.
 DR EMBL: U52159; AAC50622.1; JOINED.
 DR EMBL: U52160; AAC50622.1; JOINED.
 DR EMBL: U52161; AAC50622.1; JOINED.
 DR EMBL: U52162; AAC50622.1; JOINED.
 DR EMBL: U52163; AAC50622.1; JOINED.
 DR EMBL: U52164; AAC50622.1; JOINED.
 DR EMBL: M53994; AAA36755.1; -;
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.

DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR PDB: 1CA9; 12-APR-99.
 DR MIM: 191191; -;
 DR Interpro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR ProDom: PD000771; TNFR_c6; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00652; TNFR_NGFR_2; 4.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Phosphorylation; Pharmaceutical; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 461
 FT DOMAIN 23 257
 FT TRANSMEM 288 287
 FT DOMAIN 288 461
 FT REPEAT 39 76
 FT REPEAT 77 118
 FT REPEAT 119 162
 FT REPEAT 163 201
 FT DISULFID 40 53
 FT DISULFID 54 67
 FT DISULFID 57 75
 FT DISULFID 78 93
 FT DISULFID 96 110
 FT DISULFID 100 118
 FT DISULFID 120 126
 FT DISULFID 134 143
 FT DISULFID 137 161
 FT DISULFID 164 179
 FT CARBOHYD 171 171
 FT CARBOHYD 193 193
 FT CONFLICT 141 141
 FT CONFLICT 196 196
 FT CONFLICT 363 363
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECB67636F CRC64;
 Query Match 14.1%; Score 217; DB 1; Length 461;
 Best Local Similarity 26.0%; Pred. No. 2.8e-08;
 Matches 74; Conservative 29; Mismatches 108; Indels 74; Gaps 13;
 QY 12 PCAALLLLGLGSLTVGLGCV-----GTY-----PSNDRCHCEPRGNG 51
 DB 3 PAVMAALVAGLEMAAALPAQVAFTYAPRPGSTCRLEXYDDTAQMCCSKSPGQH 62
 QY 52 MVSRCRSQNTVCRPCGPGFYNDVSSKPKCKPCTWNLRSQSPR--KQLCTATQDTVCRC 109
 DB 63 AKVFCRTSDTYDSCEDSDSTYQLMNVF--ELSGSGSCSSQVETQACTREONRICTC 120
 QY 110 RAG-----TQPLDSTYKPG-----VDCAPCPGHS--PGDNQACK 142
 DB 121 RCGWYCALSKQECRYCALRCRPGFVARPQETSDVYCKRCACPGTFSNTTSTDICR 180
 QY 143 PPTNCTLAKHNTLQPAASNSDAICEDRDPAPQPOFOTQGPRA---RPTTV--QPTFEMP 196
 DB 181 PHQICNVVA---IPGNASRDVAVC---TSTPSRSMAGVAILDPVSTFSQHTQPPR 231
 QY 197 RTSQGPSTR-----PVEVPGRAVVAIIGLGLVLR--LGPLAI 233
 DB 232 EPTASTSTFLPMGSPRAEGSTGDPALPVGLIVGTALGLIIT 276
 RESULT 10
 TR16_RAT STANDARD; PRT; 425 AA.
 AC P07174;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)

(p75 ICD) (low affinity neurotrophin receptor p75NTR).
 NGFR OR TNFRSF16.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE=67115859; PubMed=1027580;
 RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
 RT "gene transfer and molecular cloning of the rat nerve growth factor
 RT receptor.";
 RL Nature 325:593-597(1987).
 RN [2]
 RN SEQUENCE OF 1-22 FROM N.A.
 RP TISSUE=Liver;
 RC MEDLINE=93077038; PubMed=1446821.
 RA Metts M., Timmusk T., Allikmets R., Saarma M., Persson H.;
 RT "Regulatory elements and transcriptional regulation by testosterone
 RT and retinoic acid of the rat nerve growth factor receptor promoter.";
 RL Gene 121:247-254(1992).
 RN [3]
 RN STRUCTURE BY NMR OF 334-418.
 RX MEDLINE=97449145; PubMed=9305641;
 RA Lieplish E., Ilag L.L., Olling G., Ibanez C.F.;
 RT "NMR structure of the domain of the p75 neurotrophin receptor.";
 RL EMBO J. 16:4999-5005(1997).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,
 CC AND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF
 CC NEURAL CELLS.
 CC -1- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: X05137; CAA28783.1; -;
 DR EMBL: X61269; -; NOT_ANNOTATED_CDS.
 DR PIR: A26431; A26431.
 DR PDB: 1NGR; 29-JUL-97.
 DR InterPro: IPR000488; Death.
 DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00531; death; 1.
 DR Pfam: PF00020; TNFR_C6; 4.
 DR SMART: SM00005; DEATH; 1.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00650; TNFR_NGFR_2; 4.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KM Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 KM Phosphorylation; Signal; Apoptosis; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 425
 FT
 FT DOMAIN 30 251 TUMOR NECROSIS FACTOR RECEPTOR
 FT TRANSMEM 252 273 SUPERFAMILY MEMBER 16.
 FT DOMAIN 274 425 EXTRACELLULAR (POTENTIAL).
 FT REPEAT 32 65 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 67 106 TNFR-CYS 1.
 FT REPEAT 109 147 TNFR-CYS 2.
 FT REPEAT 149 189 TNFR-CYS 3.
 FT DOMAIN 354 419 TNFR-CYS 4.
 FT DOMAIN 198 249 DEATH.
 FT DISULFID 33 44 SER/THR-RICH.
 FT DISULFID 45 58 BY SIMILARITY.
 FT BY SIMILARITY.

FT DISULFID 48 65 BY SIMILARITY.
 FT DISULFID 68 84 BY SIMILARITY.
 FT DISULFID 87 100 BY SIMILARITY.
 FT DISULFID 90 108 BY SIMILARITY.
 FT DISULFID 110 123 BY SIMILARITY.
 FT DISULFID 126 139 BY SIMILARITY.
 FT DISULFID 129 147 BY SIMILARITY.
 FT DISULFID 150 165 BY SIMILARITY.
 FT DISULFID 168 181 BY SIMILARITY.
 FT DISULFID 171 189 BY SIMILARITY.
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 425 AA; 45432 MW; B2E152D94D3827F8 CRC64;
 Query Match 14.08; Score 216; DB 1; Length 425;
 Best Local Similarity 29.68; Pred. No. 3e-08;
 Matches 83; Conservative 29; Mismatches 94; Indels 74; Gaps 15;
 QY 6 RRLGPGCAA-----LLLLGLST-----VTGLHCVGDPYPSNDRCHCPRGNGM 52
 DB 2 RRAG-AACSAADRLLRLLLLLVSSGCAKETCTGL-----YHSECCKACNLGEGV 54
 QY 53 VSRCSRSQNTVCRCGPGR-YNDVVS-SKPKPCTWC-NLNSGERRKOLCTATOPTVCRC 109
 DB 55 AOPCGANG-TVCEPCLDNVTFSDVVSATEPKCTEGLGDSMAP--CYEADAVCRC 110
 QY 110 RAGTQPLDSY-----KPYDCAPCPGPHSPGDNOA--CKPPTN 146
 DB 111 AVGYQDETHGHCACSVCEVSGLVFSCODKNTVCECEGTVSDANHVDPCLPTV 170
 QY 147 CTLAGKHTLOPASNSDAICED-----RPPAPTPQETGPPAPPTVQPT 192
 DB 171 CE-DTERLRECTPMADACEEIERGMIPRSTPPGSGSTAPSTQDEPVEPQDL-VST 228
 QY 193 EAMPRTSQGPSTPYE-----VPGRAVAAILGLGV 224
 DB 229 VADWTYVWGSSQPVYRTGTDTNLIPVYCSTLAAVVGLV 268
 RESULT 11
 TR16-CHICK STANDARD; PRT; 416 AA.
 ID TR16-CHICK
 AC P18519;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
 DE affinity nerve growth factor receptor) (NGF receptor) (gp80-LNGFR)
 DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
 GN NGFR OR TNFRSF16.
 OS Gallus gallus (chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RN SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=90166579; PubMed=2560385;
 RX Large T.H., Weskamp G., Heider J.C., Radeke M.J., Misko T.P.,
 RA Shooter E.M., Reichardt L.F.;
 RT "Structure and developmental expression of the nerve growth factor
 RT receptor in the chicken central nervous system.";
 RL Neuron 2:1125-1134(1989).
 RN [2]
 RN SEQUENCE OF 21-416 FROM N.A.
 RX MEDLINE=90152140; PubMed=2154393;
 RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;
 RT "Structure and developmental expression of the chicken NGF receptor.";
 RL Dev. Biol. 137:287-304(1990).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,
 CC AND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF

CC NEURAL CELLS (By similarity).

CC -1- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.

DR PIR: J00006; J00006.

DR PIR: A60504; A60504.

DR HSSP: P07174; INGR.

DR InterPro: IPR000488; Death.

DR InterPro: IPR001368; TNFR_c6.

DR Pfam: PF00531; death. 1.

DR Pfam: PF00020; TNFR_c6; 4.

DR SMART: SM00005; DEATH; 1.

DR SMART: SM00208; TNFR; 3.

DR PROSITE: PS00652; TNFR_NGFR.1; 3.

DR PROSITE: PS00500; TNFR_NGFR.2; 3.

DR PROSITE: PS00017; DEATH_DOMAIN; 1.

DR Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat; Phosphorylation; Signal; Apoptosis.

KM SIGNAL 1 19

FT CHAIN 20 416

FT SIGNAL 1 19

FT DOMAIN 29 239

FT TRANSMEM 240 261

FT DOMAIN 262 416

FT REPEAT 23 57

FT REPEAT 58 99

FT REPEAT 100 138

FT REPEAT 140 180

FT DOMAIN 188 236

FT DOMAIN 24 35

FT DISULFID 36 49

FT DISULFID 39 56

FT DISULFID 59 75

FT DISULFID 78 91

FT DISULFID 81 99

FT DISULFID 101 114

FT DISULFID 117 130

FT DISULFID 120 138

FT DISULFID 141 156

FT DISULFID 159 172

FT DISULFID 162 180

FT CARBOHYD 52 52

FT CONFLICT 36 36

FT CONFLICT 173 173

FT CONFLICT 276 276

FT CONFLICT 396 396

SO SEQUENCE 416 AA; 44654 MW; 6BCEAB54F4D2D56 CMC64;

Query Match 13.8%; Score 211.5; DB 1; Length 416;

Best Local Similarity 30.6%; Pred. No. 6e-08;

Matches 77; Conservative 23; Mismatches 101; Indels 51; Gaps 13;

16 LLLLLGLSTVGLNCVGTFTYNSDRCCHECRPGNGMYSRCRSQNTVCRPGPGF-VND 74

9 LLLLPAGPTWGSKEKCLTMYTTSGECCACNMGISGVQPCGVNQ-TVCEPLIDSVTSD 67

75 VVS-SKPCPKCTWC-NLRSGSERKQLCTAODTVCRAG--TQPLDYSK----- 120

68 TVSATPEPCFCTQCVGLHSMASAP---CVESDVAVCRCAYGYODELSSGCKSCSCVGEVF 124

121 ----PGVD-----CAPCPGHPSPGDN-QACKPWTNCTLACKHTLQPASSNSDAICEDR 169

125 GLMPCRBSDQIVCECECPGTFSDANFVDPCLPTICG-ENBVMWKETATSDACRDL 183

170 DEPAT--QOPEFGPPARTIVQ--TE-----AMPRTSGCPSTRPEV 209

184 HRRWTTHTPSSLGSDSPETITRDPTNTEGMATTLADIYTVVGSSQPVVSRGTADNLIFV 243

OY 310 PGRAVVAAILGL 221

DB 244 YCSIIAAVYVGL 255

RESULT 12

TNR3_HUMAN STANDARD; PRT; 435 AA.

AC P36941;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Lymphotoxin-beta receptor precursor (Tumor necrosis factor receptor 2 related protein) (Tumor necrosis factor C receptor).

GN LYBR OR TNFR OR TNFRSF3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_Taxid=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Liver;

RX MEDLINE=93252381; PubMed=8486360;

RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;

RT "Construction and evaluation of a hncDNA library of human 12p transcribed sequences derived from a somatic cell hybrid.";

RL Genomics 16:214-218(1993).

RN [2]

RP FUNCTION.

RX MEDLINE=94225209; PubMed=8171323;

RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,

RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;

RT "A lymphotoxin-beta-specific receptor.";

RL Science 264:707-710(1994).

CC -1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN IMMUNE DEVELOPMENT.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sdb.ch/announce/> or send an email to license@sdb-sdb.ch).

CC -----

CC EMBL: L04270; AAA36757.1; -.

DR HSSP: P25942; ICDF.

DR MIM: 600979; -.

DR InterPro: IPR001368; TNFR_c6.

DR Pfam: PF00020; TNFR_c6; 4.

DR PRODOM: PD000771; TNFR_c6; 1.

DR SMART: SM00208; TNFR; 4.

DR PROSITE: PS00652; TNFR_NGFR.1; 2.

DR PROSITE: PS00500; TNFR_NGFR.2; 3.

KM Receptor; Transmembrane; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 30

FT CHAIN 31 435

FT DOMAIN 31 227

FT TRANSMEM 228 248

FT DOMAIN 249 435

FT REPEAT 42 81

FT REPEAT 82 124

FT REPEAT 125 168

FT REPEAT 169 211

FT DISULFID 43 58

FT DISULFID 59 72

FT DISULFID 62 80

FT DISULFID 83 98

FT DISULFID 101 116

FT DISULFID 104 124

FT DISULFID 126 132

FT DISULFID 139 148

BY SIMILARITY.

DT 16-QC7-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 9 precursor (4-1BB
DE ligand receptor) (T-cell antigen 4-1BB) (CD137 antigen).
GN TNFRSF9 OR ILA OR LY63 OR CD137 OR CD137.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090.
RN [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=89184547; PubMed=2784565;
RA Kwon B.S., Weissman S.M.;
RT "cDNA sequences of two inducible T-cell genes."
RL Proc. Natl. Acad. Sci. U.S.A. 86:1963-1967(1989).
RN [2]
RN RP SEQUENCE FROM N.A.
RC STRAIN=BA16/C.
RC MEDLINE=94179805; PubMed=8133039;
RA Kwon B.S., Kozak C.A., Kim K.R., Pickard R.T.;
RT "Genomic organization and chromosomal localization of the T-cell
RT antigen 4-1BB."
RL J. Immunol. 152:2256-2262(1994).
RN [3]
RN RP CHARACTERIZATION AND SEQUENCE OF 25-29.
RX MEDLINE=93139510; PubMed=7678621;
RA Pollok K.E., Kim Y.-J., Zhou Z., Hurtado J., Kim K.K., Pickard R.T.,
RA Kwon B.S.;
RT "Inducible T cell antigen 4-1BB. Analysis of expression and
RT function."
RL J. Immunol. 150:771-781(1993).
CC -I- FUNCTION: RECEPTOR FOR THE PUTATIVE CYTOKINE 4-1BBL. POSSIBLY
CC ACTIVE DURING T CELL ACTIVATION.
CC -I- SUBUNIT: PRINCIPALLY AN HOMODIMER, BUT ALSO FOUND AS A MONOMER.
CC ASSOCIATES WITH P56-LCK.
CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
CC -I- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T-CELLS.
CC -I- INDUCTION: OPTIMAL BY PMA AND IONOMYCIN.
CC -I- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>).
CC Or send an email to license@isb-sib.ch.
CC -----
DR EMBL; J04492; AAA40167.1; -;
DR EMBL; U02567; AAA93113.1; -;
DR PIR; B32393; B32393.
DR HSSP; P25942; 1CDF.
DR MGD; MG1:1101059; tnfrsf9.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 1.
DR SMART; SMO0208; TNFR. 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00505; TNFR_NGFR_2; FALSE_NEG.
DR Receptor; Glycoprotein; Repeat; Signal; Transmembrane.
KW SIGNAL
FT 1 24
FT CHAIN 25 256
FT
FT TUMOR NECROSIS FACTOR RECEPTOR
FT SUPERFAMILY MEMBER 9.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.
FT CYTOPLASMIC (POTENTIAL).
FT TNFR-CYS 1.
FT REPEAT 17 45
FT REPEAT 46 85
FT REPEAT 86 117
FT REPEAT 118 159
FT CARBOHYD 128 128
FT CARBOHYD 138 138
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SEQUENCE 256 AA; 27598 MW; 93A1D003C60813C4 CRC64;

```

Query Match 13.2%; Score 202.5; DB 1; Length 256;
Best Local Similarity 25.4%; Pred. No. 1.6e-07;
Matches 64; Conservative 35; Mismatches 94; Indels 59; Gaps 12;

OY 43 CHECRPGNWNVSRGSRSONYCRPGCPGFYNDVSSKPKCKPCTMCLNLSGSR-KQLSTA 101
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB 28 CDNCCPGPT-----FCRKYNPYKSCBPSTFSGIGQPMCNICRNC--AGYFRFKPCSS 79

OY 102 TQDYVCRCRAG-----TOPLDYKKGVD-----CAPRGRHSPDNO-ACKPMTNC 147
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB 80 THNACECEIEGFHCLGPGCTKCEKRCRGGQELTKGCKTCSLGTTNDONGVCSRPATNC 139
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

OY 148 TLAKHTLQPASSNSSDAICEDRDPARPOTQGRPARPTVQRTAMPRTSGPSTBPV 207
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB 140 SLDGSRVLTGKGTETEDVVC-----GPPV--VSPSPSTITSVPEGG----- 178
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

OY 208 EYVGRRAVAAT-LGLGLVGLGLGRLATLLAL-LLRQRRLPRDHRP----- 254
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB 179 --PGHSLQVLTFLFALYSALLALIFITLLFSLVKWIKRKRPHLEKQPFKTKTGAOE 236
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|

OY 255 GGSFRTPIOE 266
    |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::| |::|
DB 237 DACSCRCPEE 248

RESULT 15
TRIB-MOUSE STANDARD: PRT: 474 AA.
AC P25119; P97893;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor 2 precursor (TNF-R2) (p75).
GN TNFRSF1B OR TNFR2 OR TNFR-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
[1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=9118785; PubMed=1849278;
RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
RA Wong G.H., Chen E.Y., Goeddel D.V.;
RT "Cloning and expression of cDNAs for two distinct murine tumor
RT necrosis factor receptors demonstrate one receptor is species
RT specific."
RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
[2]
RN RP SEQUENCE FROM N.A.
RX MEDLINE=91246168; PubMed=1645445;
RA Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
RA Copeland N.G., Jenkins N.A., Smith C.A.;
RT "Molecular cloning and expression of the type 1 and type 2 murine
RT receptors for tumor necrosis factor."
RL Mol. Cell. Biol. 11:3020-3026(1991).
[3]
RN RP SEQUENCE OF 1-26 FROM N.A.
RC STRAIN=ND;
RA Jacob C.O., Liu J.;
RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
[4]
RN RP SEQUENCE OF 1-22 FROM N.A.
RC TISSUE=Liver;
RC Kissomergis M., Fellows R., Feldmann M., Chernaiovsky Y.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way

```

CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
or send an email to license@isb-sib.ch).

DR EMBL; M60469; AAA39752.1; -;
DR EMBL; M59378; AAA40463.1; -;
DR EMBL; U39488; AAA85021.1; -;
DR EMBL; X87128; CAA60618.1; -;
DR PIR; B38634; B38634.
DR HSSP; P19438; INCF.
DR MGD; MGI:131483; Tnfisflb.
DR InterPro; IPR01368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 22
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 259 288 POTENTIAL.
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 77 TNFR-CYS 1.
FT REPEAT 78 119 TNFR-CYS 2.
FT REPEAT 120 164 TNFR-CYS 3.
FT REPEAT 165 203 TNFR-CYS 4.
FT DISULFID 40 54 BY SIMILARITY.
FT DISULFID 55 68 BY SIMILARITY.
FT DISULFID 58 76 BY SIMILARITY.
FT DISULFID 79 94 BY SIMILARITY.
FT DISULFID 97 111 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 13.2%; Score 202.5; DB 1; Length 474;
Best Local Similarity 25.1%; Pred. No. 2.8e-07;
Matches 68; Conservative 36; Mismatches 86; Indels 81; Gaps 14;

QY 42 CCHGCRPENGAVSRCSRSQNTVCRCRGFYNDVYSKPKRCPTWCNLRSGSERKOL--C 99
DB 54 CCACCPPEQYVYKFCNKTSDTVACADCEASMTQVWNQ--FRTCLSCSSCTTDQVEIRAC 111
QY 100 TATQDTVCRCRAG-----TQPLDSYKPG-----VDCAPCPGHE 133
DB 112 TKQGNRVACACEGRYCAKHTHSGSCROCMRLSKCPGFGVASSRAPNGNVLCACAPGTF 171
QY 134 S--PEDNACRPWTNCTLAGKHTLQPASNSSDAICEDRDP---PAT---QPOETQGP 182
DB 172 SDTSSITVYCRPHRICSTILA---IPGNASTDVCAPESPRLSAIPRLVYSQPEPTRS- 226
QY 183 PARPTVOPTTEAMPTSGPS-----TRPV---EVPGRANAATLIGLIVGLIGLPLAI 233
DB 227 -----QPLDQEPSPSQPTSLTSLGSPTEBOSTKGGIS---LPIGLIVGTVSLGLL 275
QY 234 LLAALY-----LLRRDQLP--PD 249
DB 276 MLGLVNCITIVQRKKKPSCLQBDAAKVPHPD 306

Search completed: June 18, 2002, 14:28:29
Job time: 223 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:24:01 ; Search time 26.53 Seconds
(without alignments)
1806.242 Million cell updates/sec

Title: US-09-852-845-2
Perfect score: 1538
Sequence: 1 MCVGARRLRGPCALLLLG.....SFRTPIOEQADAHSTLAKI 277

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

1: SPREMBL_19:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phage:*
11: sp_plant:*
12: sp_protent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*
16: sp_virus:*
17: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	924	60.1	267	6 002764	002764 oryctolagus
2	229.5	14.9	276	13 09DD2	09dd22 gallus gall
3	226	14.7	300	4 095407	095407 homo sapien
4	216	14.0	425	4 016042	016042 homo sapien
5	212.5	13.8	417	11 0920W1	0920W1 mus musculu
6	211.5	13.8	260	11 099NE0	099NE0 mus musculu
7	205.5	13.4	433	11 0912M6	0912M6 rattus norv
8	204.5	13.3	401	13 09PRG7	09PRG7 xenopus lae
9	203.5	13.2	169	11 09JKE0	09JKE0 rattus norv
10	201.5	13.1	459	11 062327	062327 mus musculu
11	194.5	12.6	283	4 096J31	096J31 homo sapien
12	193.5	12.6	222	11 099NE1	099NE1 mus musculu
13	193.5	12.6	234	11 099NE2	099NE2 mus musculu
14	191.5	12.5	430	6 09N092	09N092 macaca fasc
15	190.5	12.4	283	6 09XS28	09XS28 cercopithec
16	188	12.2	482	11 088734	088734 mus musculu

17	182.5	11.9	430	4 096924	096924 homo sapien
18	181.5	11.8	203	4 09BYU0	09BYU0 homo sapien
19	181.5	11.8	430	4 096J01	096J01 homo sapien
20	178	11.6	387	13 09PYD4	09PYD4 xenopus lae
21	174	11.3	401	4 000300	000300 homo sapien
22	173	11.2	203	11 099NE3	099NE3 mus musculu
23	171	11.1	327	11 09DCQ1	09DCQ1 mus musculu
24	171	11.1	461	11 091Y93	091Y93 rattus norv
25	171	11.1	461	11 091V30	091V30 rattus norv
26	167.5	10.9	651	13 098SM6	098SM6 gallus gall
27	164.5	10.7	186	12 072735	072735 compox viru
28	162	10.5	186	12 09YBP7	09YBP7 compox viru
29	160.5	10.4	372	4 09UNP4	09UNP4 homo sapien
30	158.5	10.3	438	13 09DFV0	09DFV0 brachydanio
31	157.5	10.2	186	12 09WJB4	09WJB4 vaccinia vi
32	157.5	10.2	655	11 09EPY5	09EPY5 mus musculu
33	157.5	10.2	655	11 091XN9	091XN9 mus musculu
34	157.5	10.2	655	11 091W77	091W77 mus musculu
35	155.5	10.1	186	12 091IR5	091IR5 vaccinia vi
36	154	10.0	655	4 075509	075509 homo sapien
37	152.5	9.9	316	12 057092	057092 ectromelia
38	152	9.9	401	11 008727	008727 rattus norv
39	151.5	9.9	320	12 057300	057300 ectromelia
40	151.5	9.9	320	12 057091	057091 ectromelia
41	151	9.8	401	11 008712	008712 mus musculu
42	150.5	9.8	320	12 057079	057079 compox viru
43	149.5	9.7	349	12 089118	089118 variola vir
44	147.5	9.6	348	12 057277	057277 monkeypox v
45	147.5	9.6	348	12 057103	057103 monkeypox v

ALIGNMENTS

RESULT 1
ID 002764 PRELIMINARY; PRT; 267 AA.
AC 002764;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 0X40 PRECURSOR (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CHB:HM;
RA Isono T., Seto A.;
RT "Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed T cell lines.";
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB003911; BAA20059.1; -.
DR HSSP; P25942; ICDF.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR ProDom; PD000771; TNFR_c6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Signal.
FT NON_TER
FT SIGNAL
FT CHAIN
SQ SEQUENCE 267 AA; 28489 MW; AB84CD3173C9500B CRC64;

Query Match 60.1%; Score 924; DB 6; Length 267;
Best Local Similarity 67.3%; Pred No. 6.6e-77;
Matches 177; Conservative 23; Mismatches 59; Indels 4; Gaps 2;
QY 15 ALLILGLSTVYGLHCVDYTPSNDRCCHCRPGNGMVSRCSSQNTVCRCPCGPGFYND 74

```

Db 9 ALLLGLLGAEPDPDCTVDTYGGGRCLECGPGYMWSCNRSODTICHPEPGFYNE 68
Oy 75 VVSSKPCRCCTOCNLRSGSERKOLCTATODTCRCRAGTODPLDSTYRGVDCAPCPGHS 134
Db 69 AVNYQACRCKCTOCNLRSGSERKOLCTATODTCRCRAGTODPLDSTYRGVDCAPCPGHS 128
Oy 135 PGDNQACRCKCTOCNLRSGSERKOLCTATODTCRCRAGTODPLDSTYRGVDCAPCPGHS 194
Db 129 EGNRRACRCKCTOCNLRSGSERKOLCTATODTCRCRAGTODPLDSTYRGVDCAPCPGHS 188
Oy 195 WRTSGPSTRVEYVGGGAVALIGLGLVLLGLLALLYLRLRQRLPDAHKRP 254
Db 189 WRTSGPSTRVEYVGGGAVALIGLGLVLLGLLALLYLRLRQRLPDAHKRP 244
Oy 255 GGSFPTPIOEQADAHSTLAKI 277
Db 245 GGSFPTPIOEQADAHSTLAKI 267

```

```

RESULT 2
O9DDD2 PRELIMINARY: PRT: 276 AA.
AC O9DDD2:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HUMAN CD40-HOMOLOGUE.
GN TNFSF5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tregaster C.A.;
RL Thesis (2001), University of Reading, Reading, UNITED KINGDOM.
DR EMBL; AJ293700; CAC20218.1; -.
DR HSP; P25942; ICDF.
DR InterPro; IPR001005; MYB_DNA_bind.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

```

Query Match 14.9%; Score 229.5; DB 13; Length 276;
 Best Local Similarity 27.1%; Pred. No. 2.9e-13;
 Matches 74; Conservative 25; Mismatches 97; Indels 77; Gaps 10;

```

Oy 7 RUGRGCAALLLLGLGLSVTLGHCVDTPYNDRCRCHRCNGVSCNSQNTVCRP 66
Db 3 RUGLGALLLGLLGGC-QPGDAVNGSDKOYEHRGCCNRCQPEKRIASCNPTEDSVCRP 61
Oy 67 CGPGFY-NDVSSKPCRCCTOCNLRSGSERKOLCTATODTCRCRAGTODPLDSTYRGVDCAPCPGHS 118
Db 62 CENGOYQHSMTKEHRCTPHEICEDNAGLLVKKGNATHNTVQCGRAGMHCSDASQCTVE 121
Oy 119 ---YRGRV-----DCARCPGHS--PEDNACRCKCTOCNLRSGSERKOLCTATODTCRCRAGTODPLDSTYRGVDCAPCPGHS 160
Db 122 NEPCQKGFVAVAMEARMTSPCEPACETFSNVSKTEPCHEFTWSCHEKGLVKKVGTN 181
Oy 161 SSDAICEDDP-----PATOPET-----OGP-----PARPITV 189
Db 182 TSDVCESSRSLSLVITTAAYTCLVGLICVHTDLRRRGKQAEAPRELVTQ 241
Oy 150 OPTAMPRTSGPSTRVEP-----GGRAYA 216
Db 242 QPFE-----VDFPQETLLGGQPA 261

```

```

RESULT 3
O95407 PRELIMINARY: PRT: 300 AA.
AC O95407:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE DECOR RECEPTOR 3 (M68) (M68C) (M68E) (DJ583p15.1.1) (TUMOR NECROSIS
DE FACTOR RECEPTOR SUPERFAMILY, MEMBER 6B, DECOR).
GN DCR3 OR TR6 OR TNFRSF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-9087326; Pubmed-9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Borstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE-BLOOD:
RX MEDLINE-99253915; Pubmed-10318773;
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA TISSUE-PANCREAS:
RX MEDLINE-20122600; Pubmed-1065513;
RA Bai C., Connolly B., Metzger M.L., Hillard C.A., Liu X., Sandig V.,
RA Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RA TISSUE-LUNG CARCINOMA, LARGE CELL UNDIFFERENTIATED.;
RC Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF104419; AAD03056.1; -.
DR EMBL; AF134240; AAD29688.1; -.
DR EMBL; AF217796; AAF35244.1; -.
DR EMBL; AF217793; AAF33685.1; -.
DR EMBL; AF217794; AAF33686.1; -.
DR EMBL; AL121845; CAC03668.1; -.
DR EMBL; BC017065; AAH17065.1; -.
DR HSP; O14763; 1D0G.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;

```

```
Query Match 14.7%; Score 226; DB 4; Length 300;
Best Local Similarity 27.0%; Pred. No. 6.5e-13;
Matches 80; Conservative 25; Mismatches 117; Indels 74; Gaps 12;

Qy 11 GPCALLILGSLGSLVTLVLCY-----GDTPPSNDR-----CCHCRPGNGMVRCSRS 59
Db 6 GPGSLTCLVTLALPALVLPVPAVGVAEPTTYPMWDAETGERLYVCAQCPCPFVQRRCRD 65

Qy 60 QNTVCRPGCGPGFYNDVSVSKPCTWGNLRS--SEBKOLCTATQDVCRCRAG----- 112
Db 66 SPTTCGPPPHRYTGFWMY--LERCRYNVLGGEREENARACHATHNACRCRTFFFAHA 123

Qy 113 --TOPLDYKRG-----VDCAPCPGHP--SPGNOACKPWTNCTLAKHTLQ 156
Db 124 GFCLEHACSPGAGVIAGTSPQNTQCCPPTGTSASSSSSEGCPRHNCALSLALNV 183

Qy 157 PASNSSDAICEDRPPATQPOETGCPARP-----TWQPTPE 193
Db 184 PGSSSHDPLCTS--CTGFPPLSTRVPGAECECERAVIDEVAFODISIKRLQLLQALFAPE 240

Qy 194 AMPRTSGPSTRVEVPGGRAVAAILGLVIGLGPL--AIIALYLRRDQRLP 247
Db 241 GW-----GPTPR-----AGRALQLKLRRLTELIGADGALLVRLQALRYARMP 286

RESULT 4
ID 016042 PRELIMINARY; PRT; 425 AA.
AC 016042.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DR 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytochrome 2:231-237(1990).
DR EMBL: S63368; AAB19824.2; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 4.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER
SQ SEQUENCE 425 AA; 44608 MW; 1B24A97E3AD4CF9F CRC64;
```

```
Query Match 14.0%; Score 216; DB 4; Length 425;
Best Local Similarity 28.1%; Pred. No. 7.8e-12;
Matches 66; Conservative 26; Mismatches 89; Indels 54; Gaps 11;

Qy 42 CCHCRPGNGMVRCSRSQNTVCRPGCGFYNDVSVSKPCKRCCTWGNLRSGER--KOLC 99
Db 17 CCSKSPGQHAQVFTKTSIDVYCDSCEDSTYQILMNWVP--ECLSCGRSSDQVETQAC 74

Qy 100 TATQDVCRCRAG-----TOPLDYKRG-----VDCAPCPGHPHS 134
Db 75 TREQNRICTCRPGMYCALSKQEGCRLCAPLRKCRPGFVGARPGTSDVYKPCAPGTFHS 134

Qy 135 --PGNOACKPWTNCTLAKHTLQPASNSSDAICEDRPPATQPOETGCPA---RPTT 188
Db 135 NTTSSTDICRPHQICNVVA---IPGNASMDAVC-----TSTSPTRSMAPGAVHLPPQVYS 185

Query Match 13.8%; Score 212.5; DB 11; Length 417;
Best Local Similarity 30.2%; Pred. No. 1.6e-11;
Matches 78; Conservative 27; Mismatches 98; Indels 55; Gaps 14;

Qy 16 LLLILGLSTVYGLH-CVGDTPPSNDRCHCRPGNGMVRCSRSQNTVCRPGCGF-YN 73
Db 9 LLLILGLVSGFGAKETCSGMTYHSGECCACNLGEGVAQPCGANQ-TVCEPCLDLSVTFHS 67

Qy 74 DVVS-SKPKPCTWC-NIRSGSERKQLCTATQDVCRCRAGTQPLDSY----- 119
Db 68 DVVSATRPCKPCTECLGLGDSMSAP---CYEADDAVCKRSGYGYQDEEGRCAACSYCVG 124

Qy 120 -----KPGVDCAPCPGHPSPGDQA--CKPWTNCTLAKHTLQPASNSSDAICED 168
Db 125 SGLVFSQDKQNTVCECEGEGYTSDEANHVDCPLCTVCE-DTERQLRRECTPMADAECDE 183

Qy 169 -----RDP-----ATQP--QETQGPAPARITYQPTAMRPTSOGSPSTRVE----- 208
Db 184 IPRMWRTRSPREGSDVTTTPSTQDEAPAPERDL-IASIVADVTTVTYMGSSQDPVVTGRAD 242

Qy 209 --VPGRAVAAILGLV 224
Db 243 NLIPVYSILAIVVGLV 260

RESULT 6
```

```

099NE0
ID 099NE0 PRELIMINARY; PRT; 260 AA.
AC 099NE0;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE CD40 TYPE V ISOFORM.
GN CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2111710; PubMed=1117023;
RA "Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
DR EMBL; AJ401390; CAC29430.1; -.
DR HSSP; P25942; 1CDE.
DR InterPro; IPR001005; MYB_DNA_bind.
DR InterPro; IPR001865; Ribosomal_S2.
DR InterPro; IPR001368; TNR_C6.
DR Pfam; PF00020; TNR_C6; 4.
DR ProDom; PD000771; TNR_C6; 1.
DR SMART; SM00208; TNR; 4.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
DR PROSITE; PS00652; TNR_NGFR_1; 1.
DR PROSITE; PS00050; TNR_NGFR_2; 4.
SQ SEQUENCE 260 AA; 28895 MW; 57ASBACE8CF2F546 CRC64;

```

```

Query Match 13.8%; Score 211.5; DB 11; Length 260;
Best Local Similarity 27.2%; Pred. No. 1.2e-11;
Matches 59; Conservative 27; Mismatches 68; Indels 63; Gaps 10;

```

```

QY 26 VVGLH-----CVGDTYPSNDRCHRCPRGNGVSRCSQNTVCRPGGPFYNDVSSK 79
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 15 LVAHVGOCVTSKDKYLDHGGCCDLCOPGSRRLTSHCTALEKTQCHPCDSGFSQAQMBE 74
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 -PCKPCTWGNLNGSERRKQCTATODTVCRCRAG----- 112
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 75 IRCHOHRCHEPNOGLRVKKEGTAEISTVCTCKEGQHTSKDCBACQHPICPGFVMEH 134
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 -TOPLDYKPGVDCAPRGHSPGDNQA-----CKPWTNCTLAGKHTLPASNSSDAIC 166
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 AETETDTV-----CHPCPYGFES---NQSLEPKCYPMWSCEDKNLEVLQKTSQINVIC 186
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 E-----DRD--PRATQ---DQETGPP---ARPI 187
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 187 EKVVKKKDNEMLPAAARQDDQEMEDYPGHNTAAIV 223
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 7
Q912M6 PRELIMINARY; PRT; 433 AA.
ID 0912M6;
AC 0912M6;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY;
RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat p60
capillary endothelial cells and participate in TNF-alpha transport

```

```

RT through the blood-brain barrier.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF420214; AAL16021.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

```

```

Query Match 13.4%; Score 205.5; DB 11; Length 433;
Best Local Similarity 26.8%; Pred. No. 7.2e-11;
Matches 68; Conservative 34; Mismatches 89; Indels 63; Gaps 13;

```

```

QY 42 CCHCRPBGNGVSRCSRSQNTVCRPGGPFYNDVSSKPKPCPTWGNLNGSERRKQ--C 99
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 34 CCAKCPBGYAKHFCMKTSPTVCADCAAGFQVMNH--LHTCLSCSSSCSDQVETVHNC 91
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 TATQDTVCRCRAGTQPLDSI-----KPG-----VCCAPC 128
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 92 TKQNRVACANA-----DSYCALKLHSGNCRQCKMLSKCGPGVARSRTSNQVICSAC 146
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 PCGHFS--PGDNQACKPWTNCTLAGKHTLPASNSSDAICEDRP--PATQPOETGPPAR 185
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 147 AGETFSDTSSPTVCAPHRICSLA----IPGNASTDAVCASPTPSAVPRITVYSQE 202
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 PTVQPTAMPRTSGP-----STRPYE--VPGGRAVAAILGLIVLGL--LGPLAIL 234
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 203 PRRSQGMDDEPGSPQPHIVLSGSRPIIEPSTIGIS---LPGLIVGLTFLGLGLMG 258
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 LA-LYLRRDQRLP 247
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 259 LANCFTLVORKKRP 272
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

RESULT 8
Q9PRG7 PRELIMINARY; PRT; 401 AA.
ID 09PRG7;
AC 09PRG7;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE P75 NEUROTHROPHIN RECEPTOR A-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodidae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hutson L.D., Richards A.P., Bothwell M.;
RT "Life and death in the developing Xenopus retina: The role of the p75
neurotrophin receptor.";
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172400; AAD51031.1; -.
DR EMBL; AF172399; AAD51030.1; -.
DR HSSP; P07174; INGR.
DR InterPro; IPR000488; Death.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001368; TNR_C6.
DR Pfam; PF00531; death_1.
DR SMART; SM00005; DEATH_1.
DR SMART; SM00208; TNR_C6; 4.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00050; TNR_NGFR_2; 3.
SQ SEQUENCE 401 AA; 43419 MW; D13BCAF7863EECF CRC64;

```

```

Query Match 13.3%; Score 204.5; DB 13; Length 401;

```

[illegible]

Db	75	INCHHRRHCELNGSLQVYKKEGTAVSDTVCTCKEGSHCAKRECEFCACQHRPGCPGGVQM	134
Qy	113	-TOPLDSYKPGVDCAPCEPGEHSPGDN--QACKPWTNC	147
Db	135	ATETEDTV-----COPCPVGFSPSSSSLPKCKHPWTSC	167
RESULT	10		
ID	062327	PRELIMINARY;	PRT; 459 AA.
AC	062327;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DE	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DF	MURINE TUMOR NECROSIS FACTOR RECEPTOR 2 PROTEIN (FRAGMENT).		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxId=10090;		
RM	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN-NOD:		
RA	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;		
RT	"Amino acid variation in the tumor necrosis factor receptor 2 is		
RL	linked to autoimmune diabetes in NOD mice."		
RM	Genomics 0:0-0(0).		
RP	[2]		
RC	SEQUENCE FROM N.A.		
RA	STRAIN-NOD:		
RT	MEDLINE=95178848; PubMed=7873884;		
RL	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;		
RT	"Allelic variation of the type 2 tumor necrosis factor receptor		
RL	gene."		
RM	Mamm. Genome 5:726-727(1994).		
DR	EMBL: X76401; CAA53981.1; -		
DR	HSP: P19438; INCF.		
DR	InterPro: IPR001568; TNFR_c6.		
DR	Pfam: PF00020; TNFR_c6; 4.		
DR	Prodom: PD000771; TNFR_c6; 1.		
DR	SMART: SM00208; TNFR: 4.		
DR	PROSITE: PS00652; TNFR_NGFR_1; 2.		
DR	PROSITE: PS50050; TNFR_NGFR_2; 3.		
KW	Receptor.		
FT	NON_TER	1	
FT	VARIANT	87	S -> T.
FT	VARIANT	93	T -> I.
FT	VARIANT	268	F -> I.
FT	VARIANT	345	S -> E.
FT	VARIANT	421	Y -> C.
SO	SEQUENCE	459 AA; 48686 MW; 6C51D2CFLC4626DF	CRC64;
Query Match	13.1%;	Score 201.5;	DB 11; Length 459;
Best Local Similarity	25.2%;	Pred. No. 1.8e-10;	
Matches	68; Conservative	34; Mismatches	89; Indels 79; Gaps 14;
Qy	42	CCHCEKPCNGMYSRCSRSNTVCRCPCGPGFYNDVYS--KPCPKPTWMLRSGSEKOLCT	100
Db	39	CCAKCPGGYVYVHFKCKTSDTYCACDCEASMTYQVWNNQPTCLSCS--SSCSTDYQVETRACT	97
Qy	101	ANQDVTGRCRAG-----TOPLDSYKPG-----VDCAPCPGHFS	134
Db	98	KQONRFVCAACEARVYCALKTHSGSCRCQMRLSKCGPGFVASSRAPDNGVILKACAPGTF	157
Qy	135	-PGDNQACPKPTNCTIAGKHTLPASNSSDAICEDRP-----PAT-----QPGTQGP	183
Db	158	DTTSTDTVCRRPHRISILA---IPGNASTDAVCAPESTPLSAIPRTLYVSGPEPTRS--	211
Qy	184	ARPIYQPEAPRPRTSGRS-----TRVY-----EYVGGRAVNAIIGLGILGLPLAII	234
Db	212	-----QPLDQERGGQSPTSLTSLGSPITIDQSKRGIS---LPILGIVGYSGLGLM	261
Qy	235	LALY-----LLRQDQRLP--PD	249

DB 262 LGLVNCFLVORRKKKPCSLQBDKAVPHVD 291

RESULT 11

Q96J31 PRELIMINARY: PRT: 283 AA.

AC Q96J31; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 14 (HERPESVIRUS ENTRY MEDIATOR).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxId=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=MELANOMA;

RA Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC002794; AA02794.1; --

KW Receptor.

SQ SEQUENCE 283 AA: 30420 MW: DFCEL46E4E024F4B CRC64:

Query Match 12.6%; Score 194.5; DB 4; Length 283;

Best Local Similarity 28.8%; Pred. No. 4.7e-10;

Matches 46; Conservative 14; Mismatches 59; Indels 41; Gaps 5;

QY 31 CVDGTPSNDRCHECRPGNGVSRCSQNTVCRPGGFFNDVVS-KPKCKPTWML 89

DB 42 CDEDEPVPSECCPKSPGVRYKACGELGTVCCEPCPGTYIAHLNGLSKLQCCMCDP 101

QY 90 RGSSEKOLCTATODTVCRAGT-----RAGTODPLDSY 119

DB 102 AMGLRASRNCSTRNNAVCGCSPEGHCTVODGDHCAACRAVATSSPGQVRQKGTESQDTL 161

QY 120 KPGVDCAPCPGHFSP-GDNOACKPWTNC-----TLAKKHT 154

DB 162 -----CONCPPTGTFSPNGTLECGQHQTCSWLTAKAGACT 196

RESULT 12

Q99NE1 PRELIMINARY: PRT: 222 AA.

AC Q99NE1; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CD40 TYPE IV ISOFORM.

GN CD40.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2111710; PubMed=11172023;

RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;

RT "Regulation of CD40 function by its isoforms generated through alternative splicing."

RT Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

RL EMBL: AJ401389; CAC29429.1; --

DR HSP: P25942; 1CDF.

DR InterPro: IPR001005; MYD_DNA_bind.

DR InterPro: IPR001865; Ribosomal_S2.

DR Pfam: PF00020; TNFR_c6; 4.

DR ProDom: PD000771; TNFR_c6; 1.

DR SMART: SM00208; TNFR; 4.

DR PROSITE: PS00037; MYB_1; UNKNOWN_1.

DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.

DR PROSITE: PS00652; TNFR_NGFR_1; 1.

DR PROSITE: PS00050; TNFR_NGFR_2; 4.

SQ SEQUENCE 222 AA: 24499 MW: EE21E6C76FB42DEF CRC64:

Query Match 12.6%; Score 193.5; DB 11; Length 222;

Best Local Similarity 26.7%; Pred. No. 4.5e-10;

Matches 48; Conservative 23; Mismatches 62; Indels 47; Gaps 6;

QY 26 VYGLH-----CVDGTPSNDRCHECRPGNGVSRCSQNTVCRPGGFFNDVVS 79

DB 15 LTAIVHLGQCVTSCDKQYLHDGQCCDLCQPSRLTSHCTALEKTQCHPCDSGERSAQMRE 74

QY 80 -PCKPTWNLRSSEKOLCTATODTVCRAG-----CKPTNCTLAGKHTLQPSNSSDAIC 112

DB 75 IRCHQHRHCEPNOGLVKKKEGTAEEDTVCTCKRGQHTSKDEACAGHTPCIRPGVME 134

QY 113 -TOPPLDSYKPGVDCAPCPGHFSPGDNQ-----CKPTNCTLAGKHTLQPSNSSDAIC 166

DB 135 ATETTDTV-----CHCPVGFFS---NQSLEPKCYPMTSCEDKNLEVLQKGTSTQTNVIC 186

RESULT 13

Q99NE2 PRELIMINARY: PRT: 234 AA.

AC Q99NE2; 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE CD40 TYPE III ISOFORM.

GN CD40.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=2111710; PubMed=11172023;

RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;

RT "Regulation of CD40 function by its isoforms generated through alternative splicing."

RT Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).

RL EMBL: AJ401388; CAC29428.1; --

DR HSP: P25942; 1CDF.

DR InterPro: IPR001005; MYD_DNA_bind.

DR InterPro: IPR001865; Ribosomal_S2.

DR Pfam: PF00020; TNFR_c6; 4.

DR ProDom: PD000771; TNFR_c6; 1.

DR SMART: SM00208; TNFR; 4.

DR PROSITE: PS00037; MYB_1; UNKNOWN_1.

DR PROSITE: PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.

DR PROSITE: PS00652; TNFR_NGFR_1; 1.

DR PROSITE: PS00050; TNFR_NGFR_2; 4.

SQ SEQUENCE 234 AA: 25747 MW: 00DB1DD38347E325 CRC64:

Query Match 12.6%; Score 193.5; DB 11; Length 234;

Best Local Similarity 26.7%; Pred. No. 4.8e-10;

Matches 48; Conservative 23; Mismatches 62; Indels 47; Gaps 6;

QY 26 VYGLH-----CVDGTPSNDRCHECRPGNGVSRCSQNTVCRPGGFFNDVVS 79

DB 15 LTAIVHLGQCVTSCDKQYLHDGQCCDLCQPSRLTSHCTALEKTQCHPCDSGERSAQMRE 74

QY 80 -PCKPTWNLRSSEKOLCTATODTVCRAG-----CKPTNCTLAGKHTLQPSNSSDAIC 112

DB 75 IRCHQHRHCEPNOGLVKKKEGTAEEDTVCTCKRGQHTSKDEACAGHTPCIRPGVME 134

QY 113 -TOPPLDSYKPGVDCAPCPGHFSPGDNQ-----CKPTNCTLAGKHTLQPSNSSDAIC 166

DB 135 ATETTDTV-----CHCPVGFFS---NQSLEPKCYPMTSCEDKNLEVLQKGTSTQTNVIC 186

```

RESULT 14
O9N092 PRELIMINARY: PRT: 430 AA.
AC O9N092:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE UNNAMED PROTEIN PRODUCT.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Cercopitheciinae; Primates; Catarrhini; Cercopitheciidae;
OC NCBI_TaxID=9541;
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,
RA Suzuki Y., Sugano S., Hashimoto K.;
RT "Isolation of full-length cDNA clones from macaque brain cDNA
RT libraries."
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB046039; BAB01621.1;
DR InterPro; IPR001368; TNFR_C6.
DR SMART; SM00208; TNFR; 1.
SQ SEQUENCE 430 AA; 45850 MW; BA8DE92593E1E859 CRC64;

```

```

Query Match 12.5%; Score 191.5; DB 6; Length 430;
Best Local Similarity 28.2%; Pred. No. 1.4e-09;
Matches 78; Conservative 30; Mismatches 94; Indels 75; Gaps 14;

```

```

OY 16 LLLGLGLSTVGLHCYGVDTYPSNDRCHCECRPGNGMVSRCSONTWCRPGCGFYNDY 75
DB 14 LMLLWPLATL-----STTLWQCPPE--EEDLNGGQITLRCPCPGTFSA 59
OY 76 VSSKPCPCCTWCLNLSGSRKQLCTATQDTVC-RCRAGTQPLDSYKP-GVDCAPCPGHE 133
DB 60 WSSSPQPHARCSLGRLE-AQVGTAQDTLGGDCWPGW----FGPMGVPRVPCQPCSM 113
OY 134 SPGDNACKPMNTCTAGKHTLQAPASNSSDAICEDRDPRATQQTQETGSPARITYQPT 193
DB 114 APLGIGHGCEWGRARRGVEVAAGSSGE-----TRQP-- 147
OY 194 AMPRTSQGPSTR---PVEYPGRAVAAILGLGLGLPLAILLALYLLRDQRLPPDA 250
DB 148 -----GNGTRAGCEPETAQAAYAIYVPVCLMGLG-----ILVCNLKR-KGYHCTA 195
OY 251 HK---PPGGG-----FRTPIQEODAHSTLAKI 277
DB 196 HKEVGPFGGGSGINPAYRT--EDVNEDTIGLVRL 230

```

```

RESULT 15
O9XS28 PRELIMINARY: PRT: 283 AA.
AC O9XS28:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HVEAS.
GN HVEAS.
OS Cercopithecus aethiops (Green monkey) (Griwet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopitheciinae;
OX NCBI_TaxID=9534;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=KIDNEY;
RC MEDLINE=99296730; PubMed=10366573;
RX Foster T.P., Chouljenko V.N., Kousoulas K.G.;
RT "Functional characterization of the HveA homolog specified by African

```

```

RT green monkey kidney cells with a herpes simplex virus expressing the
RT green fluorescence protein."
RT Virology 258:365-374(1999).
DR EMBL; AF147720; AAD37381.1;
DR HSP; 014763; 1D0G.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 3.
DR ProDom; PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;

```

```

Query Match 12.4%; Score 190.5; DB 6; Length 283;
Best Local Similarity 26.3%; Pred. No. 1.1e-09;
Matches 66; Conservative 29; Mismatches 107; Indels 49; Gaps 12;

```

```

OY 12 PCAALLLLGLGLSTVGLHCYV-----DTPSNDRCHCECRPGNGMVSRCSONTW 63
DB 16 PKADITLVLYL-TFLGSSCYAPALPSCKEDEYVPGSECCPKGPGFHVQACGEQTGY 74
OY 64 CRPCGPGFY---NDVYSSKPCPCCTWCLNLSGSRKQLCTATQDTVCRCRAGTQPLDS 119
DB 75 CEPSPGTYIAHENG---SKLQCCQCDPAMQGLRTSRNCSTYANALC----- 119
OY 120 KPGVDCAPCPPGHE---SPGDN-QACKPMNTCTAGKHTLQAPASNSSDAICEDRDPRATQ 175
DB 120 -----GSPGHFCITIQDDHCACARAYATSS-PQORVQGGTESQDTLCON-CPGRT 169
OY 176 PQTGPPPARPIVQPTTEAMPRTSQGPSTRPVEYPGRAVAAIL-GLGLVGLGLPLAIL 234
DB 170 -FSSNGTLEECQHGNCMKLVTEAGPT-----SSSRWVWMLSSSLIYIVIGLIILK 223
OY 235 LALYLLRDQR 245
DB 224 LITCVRRRSR 234

```

```

Search completed: June 18, 2002, 14:26:16
Job time: 135 sec

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:23:56 ; Search time 30.01 Seconds
(Without alignments)
1025.240 Million cell updates/sec

Title: US-09-852-845-2
Perfect score: 1538
Sequence: 1 MCVGARRLRGSPCALLLLG.....SFRPPIQEQDAHSTLAKI 277

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: A.Geneseq_032802.*
2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.*
3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.*
4: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.*
5: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.*
6: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.*
7: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.*
8: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1986.DAT.*
9: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1987.DAT.*
10: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1988.DAT.*
11: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1989.DAT.*
12: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1990.DAT.*
13: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1991.DAT.*
14: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1992.DAT.*
15: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1993.DAT.*
16: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.*
17: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.*
18: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1996.DAT.*
19: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.*
20: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.*
21: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.*
22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.*
23: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1538	100.0	277	16 AAR74737	ACT-4 cell surface
2	1538	100.0	277	16 AAR79904	ACT-4-h-1 receptor
3	1538	100.0	277	22 AAB35329	Human OX40 protein
4	1538	100.0	277	22 AAB50522	Human tumour necro
5	1496	97.3	277	16 AAR76996	Deduced sequence e
6	676.5	44.0	438	16 AAR81882	Plasmodium POC406/OX4
7	676.5	44.0	438	16 AAR48976	OX40/FC mitein. C
8	676.5	44.0	205	22 AAB66985	OX40 protein. Uni
9	675.5	43.9	206	16 AAR81881	Mouse type-II memb
10	675.5	43.9	206	16 AAR48977	Mouse OX40 extrace
11	329	21.4	56	20 AAW94649	TNF-R extracellular

12	318	20.7	58	22 AAB69201	Human TNF-R extrac
13	248.5	16.2	415	22 AAB36700	Human tumour necro
14	247	16.1	19	22 AAB69951	RANK polypeptide p
15	247	16.1	15	22 AAB68287	RANK polypeptide p
16	247	16.1	451	22 AAB08732	Human receptor act
17	247	16.1	451	22 AAB04420	Human receptor act
18	247	16.1	451	22 AAB01987	Human 9D-15C clone
19	247	16.1	532	22 AAB02025	Human RANK deletio
20	247	16.1	544	22 AAB02024	Human RANK deletio
21	247	16.1	616	19 AAB69952	NF-kB receptor act
22	247	16.1	616	19 AAB68288	NF-kB receptor act
23	247	16.1	616	21 AAY53647	A human receptor a
24	247	16.1	616	22 AAB08733	Human receptor act
25	247	16.1	616	22 AAB04421	Human receptor act
26	247	16.1	616	22 AAB01988	Human full-length
27	247	16.1	616	22 AAB66560	Human RANK protein
28	246	16.0	622	22 AAB01999	Human FEO RANK (re
29	243.5	15.8	625	22 AAB02000	Human EP RANK (re
30	243	15.8	615	20 AAB30659	Human tumour necro
31	243	15.8	616	19 AAB79233	A receptor protein
32	236	15.3	591	19 AAB69950	RANK polypeptide p
33	236	15.3	591	19 AAB68286	RANK polypeptide p
34	236	15.3	591	22 AAB08731	Human receptor act
35	236	15.3	591	22 AAB04419	Human receptor act
36	236	15.3	591	22 AAB01986	Human 9D-8A clone
37	226	14.7	300	19 AAB66102	Amino acid sequenc
38	226	14.7	300	19 AAB63622	Human tumour necro
39	226	14.7	300	20 AAY03099	Human lung TNF-rec
40	226	14.7	300	20 AAY42182	Human FLITR #1 pro
41	226	14.7	300	20 AAY17479	Mammalian tumour n
42	226	14.7	300	20 AAY06817	Human DCR3 polypep
43	226	14.7	300	20 AAW97749	Human tumour necro
44	226	14.7	300	20 AAW95082	Orphan receptor (H
45	226	14.7	300	21 AAB19335	A full length huma

ALIGNMENTS

RESULT 1	AAR74737	standard; Protein: 277 AA.
ID	AAR74737	
XX		
AC	AAR74737	
XX		
DT	21-NOV-1995	(first entry)
XX		
DE	ACT-4 cell surface receptor protein.	
XX		
KM	Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	Peptide	1..24
FT		/note= "signal peptide"
FT	Cleavage-site	22..23
FT		/note= "signal cleavage site"
FT	Cleavage-site	24..25
FT		/note= "signal cleavage site"
FT	Modified-site	146..148
FT		/note= "glycosylation site"
FT	Modified-site	160..162
FT		/note= "glycosylation site"
FT	Domain	214..240
FT		/note= "transmembrane domain"
PN	W09512673-A.	
XX		
PD	11-MAY-1995.	
XX		
PF	03-NOV-1994;	94NO-GB02415.
XX		

PR 03-NOV-1993; 93US-0147784.
 XX
 PA (BECT) BECTON DICKINSON CO.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 PI Buck DW, Engleman EG, Godfrey W;
 XX
 DR WPI: 1995-185777/24.
 DR N-PSDB; AAQ88758.
 XX
 PT Isolated ACT-4 receptor from activated T-cells - also its ligands and
 PT antibodies, useful for treating diseases of the immune system
 XX
 PS Claim 1: Fig. 5; 82pp; English.
 XX
 CC This sequence encodes the full-length cell surface receptor ACT-4
 CC isolated from activated CD4+ T-lymphocytes. The sequence may be
 CC expressed in e.g. COS-7 cells. The encoded protein, its ligands or
 CC fragments, and antibodies may be used for the treatment of transplant
 CC rejection, graft-versus-host disease, autoimmune disease, etc.
 XX
 SQ Sequence 277 AA;

Query Match 100.0%; Score 1538; DB 16; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.2e-100;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCVGARRLGRPCAAALLLGLSTVITGLHCYGDTPPSNDRCHCRPGNGVSRCSRSQ 60
 DB 1 mcvgarririgrpcaalllllgistvtgihcygdtpsndrcchecrpgngvsrcrsq 60
 OY 61 NTVCRRPGGFGFYNDVSSKPKPCCTWCNLRSGSERKQLCTATQDTVRCRAGTQPLDSYK 120
 DB 61 ntvcrrpggfyndvsskpkpcctwcnlrsgserkqlctatqdtvcrcragtqpldsyk 120
 OY 121 PGVDCAPCPGPHFHSRQDNACKPWTNCTLAGKHTLQPA NSSDAICEDBDPATQPOETQ 180
 DB 121 pgvdcapcpghfhsrpdnackpwtncclagkhtlqpasnsdalcdbdpattqpgetq 180
 OY 181 GPAPRPITVQPTPEAMPRTSOGSPTRVPEVPGRAVAAILGLGLVILGLPLAILLALYL 240
 DB 181 gpaprpitvqptpeamprtsogsptrvpevpgrravaailglglvlgllplailllalyll 240
 OY 241 RRDQRLPPDAHKKPGGSGFRTPRIOEQADAHSTLAKI 277
 DB 241 rrdqrlppdahkppgsgsfrtprlqeeqadahstlaki 277

RESULT 2

AAR79904
 ID AAR79904 standard; Protein: 277 AA.

AC AAR79904;

DT 05-MAR-1996 (first entry)

XX ACT-4-h-1 receptor sequence.

XX ACT-4: specific binding partner: sbd; B cells; lymphocyte; GVHD;
 KW graft versus host disease; immune response; transplantation;
 KW autoimmune disease; inflammation; HIV; human immunodeficiency virus;
 KW HTLV; human T lymphocyte virus; inflammatory bowel disease;
 KW screening; identification.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Cleavage-site 22..23 /note= "Possible cleavage site."

FT Cleavage-site 24..25 /note= "Possible cleavage site."

FT Modified-site 136..138

FT /label- glycosylation site.
 FT Modified-site 150..152
 FT /label- glycosylation site.
 FT Domain 204..230
 FT /label- Transmembrane domain.

XX WO9521915-A1.

XX 17-AUG-1995.

XX 06-FEB-1995; 95MO-GB00238.

XX 10-FEB-1994; 94US-0195967.

XX (GREA/) GREAVES C P.

XX (STRD) UNIV LELAND STANFORD JUNIOR.

XX Engleman EG, Godfrey W;

XX WPI: 1995-293117/38.

XX N-PSDB; AAT04048.

XX Ligand, ACT-4-L, to receptor on activated CD4 positive cells -
 XX useful in treatment of various immune diseases and conditions

XX Disclosure: Figure 5; 124pp; English.

CC ACT-4-L-1 is a specific binding partner (sbp) to the ACT-4
 CC receptor polypeptide (encoded by this sequence) on the surface of
 CC activated CD4 positive B cells. The sbp and its fragments are useful
 CC in pharmaceutical applications to modify a patient's immune response
 CC as well as having application in the treatment of transplant
 CC rejection, graft versus host disease, autoimmune disease,
 CC inflammation, infectious agents, HTLV infected cells or HIV.
 CC Specifically the sbd can be used to treat inflammatory bowel
 CC disease. The sbd can also be used for screening for immunomodulatory
 CC agents able to recognise ACT-4 and for monitoring activated CD4
 CC positive cells or inhibiting infection of CD4 positive cells.

XX Sequence 277 AA;

Query Match 100.0%; Score 1538; DB 16; Length 277;
 Best Local Similarity 100.0%; Pred. No. 1.2e-100;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCVGARRLGRPCAAALLLGLSTVITGLHCYGDTPPSNDRCHCRPGNGVSRCSRSQ 60
 DB 1 mcvgarririgrpcaalllllgistvtgihcygdtpsndrcchecrpgngvsrcrsq 60
 OY 61 NTVCRRPGGFGFYNDVSSKPKPCCTWCNLRSGSERKQLCTATQDTVRCRAGTQPLDSYK 120
 DB 61 ntvcrrpggfyndvsskpkpcctwcnlrsgserkqlctatqdtvcrcragtqpldsyk 120
 OY 121 PGVDCAPCPGPHFHSRQDNACKPWTNCTLAGKHTLQPA NSSDAICEDBDPATQPOETQ 180
 DB 121 pgvdcapcpghfhsrpdnackpwtncclagkhtlqpasnsdalcdbdpattqpgetq 180
 OY 181 GPAPRPITVQPTPEAMPRTSOGSPTRVPEVPGRAVAAILGLGLVILGLPLAILLALYL 240
 DB 181 gpaprpitvqptpeamprtsogsptrvpevpgrravaailglglvlgllplailllalyll 240
 OY 241 RRDQRLPPDAHKKPGGSGFRTPRIOEQADAHSTLAKI 277
 DB 241 rrdqrlppdahkppgsgsfrtprlqeeqadahstlaki 277

RESULT 3

AAB35329
 ID AAB35329 standard; Protein: 277 AA.

AC AAB35329;

DT 08-MAY-2001 (first entry)
XX
DE Human OX40 protein SEQ ID NO: 3.
XX
KW Human: tumour necrosis factor receptor; TR13; TR14; infection;
KW cancer; autoimmune disease; allergy; inflammatory disease;
KW graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS Homo sapiens.
XX
PN MO200105834-A1.
XX
PD 25-JAN-2001.
XX
PF 14-JUL-2000; 2000WO-US19343.
XX
PR 16-JUL-1999; 99US-0144087.
PR 18-AUG-1999; 99US-0149450.
PR 20-AUG-1999; 99US-0149712.
PR 10-SEP-1999; 99US-0153089.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Young PE.
XX
DR WPI; 2001-112682/12.
XX
XX Nucleic acids encoding 2 human tumor necrosis factor receptor
PT polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis
PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT hypohidrotic ectodermal dysplasia -
XX
XX Disclosure; Page 372-373; 418pp; English.
XX
XX The present invention provides the protein and coding sequences of the
CC human tumor necrosis factor receptors TR13 and TR14. These sequences are
CC useful in the diagnosis and treatment of many diseases, including cancer,
CC autoimmune diseases, cardiovascular disorders, allergies,
CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC infections.
XX
XX Sequence 277 AA:
SQ
Query Match 100.0%; Score 1538; DB 22; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.2e-100;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCVGARRLGRCPCAAALLLGLSTVTVGLHCYGVDTTPSNDRCCHCPCPGNGVSRCSRSQ 60
DB 1 mcvgarrrlgrpcacalllllglstvtglhcygdtyppsndrcchcpcpgngvsrcrsq 60
QY 61 NTVCRCPCGPGFYNDVSSKPCPKCTWCNLRSGSERKQLCTAODIVCRAGTQPLDSYK 120
DB 61 ntvcrcpcpgpfyndvsskpcpkctwcnlrsgsrerkqlctaodivcrtcragtqpldsyk 120
QY 121 PGVDCAPCPGPHFSPGDNQACKPMTNCTLAGKHTLOPASNSSDADICEDRDPATPOETO 180
DB 121 pgvdcapcpghfspgdnqackpmtntctlagkhtlopasnssdadicedrdpatpgetq 180
QY 181 GPPAPRTVQPEAMPRTSOGSPTRPEVPGGRANVAAILGLGLVIGLLPLAILALYL 240
DB 181 gppaprtlvqpeamprrtsogsptrpevpggravaailglglvlgllplailalyl 240
QY 241 RRDORLPPDAHKPCGSGSFRFPJOEODAHSTLAKI 277
DB 241 rrdqrlppdahkpgsgsfrfpijoeodahstlaki 277
RESULT 4
AAB50522
ID AAB50522 standard; Protein; 277 AA.
XX

AC AAB50522;
XX
DT 15-MAR-2001 (first entry)
XX
DE Human tumour necrosis factor receptor OX40 protein SEQ ID NO:12.
XX
KW Human: tumour necrosis factor receptor 5; TR1D; TNFR-5; TR5; neutrotropic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotrophic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX
XX Homo sapiens.
XX
XX MO200071150-A1.
XX
XX 30-NOV-2000.
XX
XX 18-MAY-2000; 2000WO-US13515.
XX
XX 20-MAY-1999; 99US-0135164.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Wel Y, Ruben SM, Gentz RL, Ni J;
XX
XX WPI; 2001-041051/05.
XX
XX Nucleic acid encoding a TR1D polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PT prevention of cancer, autoimmune disorders and viral infection -
XX
XX Disclosure; Fig 2; 285pp; English.
XX
XX The present invention describes the human TR1D protein (tumour necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumour necrosis factor
CC receptor 5 (TNFR-5 or TR5)). TR1D has cytostatic, immunosuppressive,
CC neurotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotrophic
CC activities, and can be used in gene therapy. The TR1D polynucleotides
CC are useful for detecting complementary polynucleotides. TR1D proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to
CC parasite, bacteria and viruses, restenosis and graft versus host disease.
CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain hematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TR1D by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TR1D
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TR1D
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis; treatment or prevention of: (a) cancer;
CC (b) autoimmune disorders; (c) diseases associated with increased
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC present sequence represents a tumour necrosis factor receptor used in
CC comparison with TR1D in the exemplification of the present invention.
XX
XX Sequence 277 AA:
SQ
Query Match 100.0%; Score 1538; DB 22; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.2e-100;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MCVGARRLGRCPCAAALLLGLSTVTVGLHCYGVDTTPSNDRCCHCPCPGNGVSRCSRSQ 60
DB 1 mcvgarrrlgrpcacalllllglstvtglhcygdtyppsndrcchcpcpgngvsrcrsq 60
QY 61 NTVCRCPCGPGFYNDVSSKPCPKCTWCNLRSGSERKQLCTAODIVCRAGTQPLDSYK 120
DB 1 ntvcrcpcpgpfyndvsskpcpkctwcnlrsgsrerkqlctaodivcrtcragtqpldsyk 120
XX

Db 61 ntvcrcpgpgfyndvsvskpckpctwcnlrsgserqkqlctatqdtvcrcragtqpldsyk 120
 Qy 121 PGVDCAPCPGHPSPGDNOACKPWTNCTLAGHTTLPASNSDAICEDRDPATQPEHQ 180
 Db 121 pyvdcapcppghfsgpdnackpwtctclagkhtclqpaanssdaicedrppatqpeq 180
 Qy 181 GPPARPIVQPTPEAWPRTSGPSTRPEVPGGRAVAAILGLIVGLPLATLLALYLL 240
 Db 181 gpparpilvqpleawprrtsqpsrtrpvevpggravaailglivglplalllalyll 240
 Qy 241 RRDQRLPPDAHKKPPGGSGFRTPIOEQADAHSTLAKI 277
 Db 241 rrdqrlppdahkkppggsfrtrpiqueadahnstlaki 277

RESULT 5
 AAR76996
 ID AAR76996 standard; Protein: 277 AA.
 AC AAR76996;
 XX
 XX 21-DEC-1995 (first entry)
 DT
 XX
 XX Deduced sequence encoded by human OX-40 cDNA.
 DE
 XX
 XX Human OX-40; activated T-cells; CD4+ T-cells; antigen;
 KW multiple sclerosis; sarcoidosis; rheumatoid arthritis; uveitis;
 KW T-cell lymphoma.
 XX
 OS Homo sapiens.
 XX
 PN W09521251-A.
 XX
 PD 10-AUG-1995.
 XX
 PF 06-FEB-1995; 95WO-GB00237.
 XX
 PR 04-FEB-1994; 94US-0192480.
 XX
 XX (WEIN/) WEINBERG A D.
 PA (CANT-) CANTAB PHARM RES LTD.
 XX
 PI Vandenbark AA, Weinberg AD;
 XX
 DR WPI: 1995-283771/37.
 DR N-PSDB: AA093257.
 XX
 XX Nucleic acid encoding an activated T-cell antigen, OX-40 - used to
 PT develop prods. for detection and therapy of conditions mediated by
 PT activated T-cells, eg. multiple sclerosis, rheumatoid arthritis, etc.
 XX
 PS Claim 3; Fig 11; 91pp: English.
 XX
 CC Antigen OX-40 is specifically expressed on the cell surface of
 CC antigen activated T-cells, especially, for example, CD4+ T-cells. A
 CC human cDNA encoding the human OX-40 homologue was cloned as follows.
 CC Using the Experimental Autoimmune Encephalomyelitis model in rats
 CC the OX-40 antigen was identified (expressed on the surface of
 CC activated autogenous-specific CD4+ T-cells present at the site of
 CC inflammation but absent on CD4+ T-cells at non-inflammatory sites)
 CC and cDNA encoding the antigen was isolated. PCR primers were
 CC designed and used to clone murine OX-40 cDNA by PCR from RNA
 CC isolated from murine CD4+ T-cells activated with concanavalin A.
 CC Then the murine OX-40 cDNA was used to probe a cDNA lambda g11
 CC library from human activated T lymphocytes to obtain human OX-40
 CC cDNA. The published patent application states that the OX-40 cDNA
 CC sequence is also in SQ ID no. 1, but this sequence is not present
 CC in the spec. A nucleic acid having the sequence in SQ ID no 1 and
 CC the polypeptide encoded by it are claimed.
 XX
 SQ Sequence 277 AA;

Query Match 97.3%; Score 1496; DB 16; Length 277;
 Best Local Similarity 97.5%; Pred. No. 1, 1e-97;
 Matches 269; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MCVGARRLRGRCPCALLLLGLISTYTGILHCVGDTYRPSNDRCHERRPENGWYRSRSRQ 60
 Db 1 mcvgarrlrgpcaallllglislvtgilhcvgdtyrpsndrcheerpngwrsrsrq 60
 Qy 61 NTVCRCGPGFYNDVSVSKPCKPCTWCNLRSGSERQQLTATQDTVCRCRAGTQPLDSYK 120
 Db 61 ntvcrcpgpgfyndvsvskpckpctwcnlrsgserqkqlctatqdtvcrcragtqpldsyk 120
 Qy 121 PGVDCAPCPGHPSPGDNOACKPWTNCTLAGHTTLPASNSDAICEDRDPATQPEHQ 180
 Db 121 pyvdcapcppghfsgpdnackpwtctclagkhtclqpaanssdaicedrppatqpeq 180
 Qy 181 GPPARPIVQPTPEAWPRTSGPSTRPEVPGGRAVAAILGLIVGLPLATLLALYLL 240
 Db 181 gpparpilvqpleawprrtsqpsrtrpvevpggravaailglivglplalllalyll 240
 Qy 241 RRDQRLPPDAHKKPPGGSGFRTPIOEQADAHSTLAK 276
 Db 241 rrdqrlppdahkkppggsfrtrpiqueadahnstlvk 276

RESULT 6
 AAR81882
 ID AAR81882 standard; Protein: 438 AA.
 XX
 AC AAR81882;
 XX
 XX 30-MAR-1996 (first entry)
 DT
 XX
 XX Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.
 DE
 XX
 KW OX40: OX40-L; cytokine; cell surface molecule; plasmid;
 KW pDC406/OX40/Fc*; membrane glycoprotein.
 XX
 OS Synthetic.
 XX
 PN US5457035-A.
 XX
 PD 10-OCT-1995.
 XX
 PF 23-JUL-1993; 93US-0097827.
 XX
 PR 23-JUL-1993; 93US-0097827.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
 XX
 DR WPI: 1995-357992/46.
 DR N-PSDB: AAT00829.
 XX
 XX New isolated DNA encoding the OX40 ligand polypeptide - also vectors
 PT and host cells, used to produce recombinant ligand used in e.g.
 PT prim. T cell culture, to modulate immune response etc.
 XX
 PS Example 2; Column 35-38; 26pp: English.
 XX
 CC This plasmid encodes an OX40/Fc antibody fragment mutein protein,
 CC and is used to express a soluble OX40/Fc mutein fusion protein for
 CC use in detecting cDNA clones encoding a OX40 ligand. The Fc
 CC fragment may be derived from human IgG1, and the plasmid may be
 CC used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell
 CC line. Culture supernatant was purified by affinity chromatography
 CC and this was used, together with labeled goat anti-human IgG to
 CC screen various cell lines.
 XX
 SQ Sequence 438 AA;

CC related activation-induced cytokine (TRANCE)/receptor activator of
CC NF-kappaB ligand (RANK) inhibitors. The method is useful for treating
CC diseases characterised by bone loss such as osteoporosis, Paget's
CC disease, metastatic bone disease, rheumatoid arthritis or periodontal
CC disease, and modulating dendritic cell maturation, T cell proliferation,
CC and/or CD40 receptor systems. The present sequence represents an
CC extracellular Cys-rich domain of a tumour necrosis factor receptor of
CC (TNF-R) superfamily member, which is used in the exemplification of
CC the present invention.

CC Sequence 58 AA:

Query Match 20.7%; Score 318; DB 22; Length 58;
Best Local Similarity 96.6%; Pred. No. 1.4e-15;
Matches 56; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 64 CRPGCGFNDVSSKPKCTMCNLRSGSERKOLCTATQ--DTVCRGAGTQPLDSY 119
DB 1 crpgpgfndvsskpkctmcnlrsgserkqlctatqdcvtccrctagtpldsy 58

RESULT 13
AAB36700

ID AAB36700 standard; Protein; 415 AA.

AC AAB36700;

DT 15-MAR-2001 (first entry)

DE Human tumour necrosis factor receptor LTR protein SEQ ID NO:6.

XX Human; tumour necrosis factor receptor 5; TRID; TNF-R5; TR5; noctropic;
KM TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KM tumour necrosis factor related apoptosis inducing ligand; vasotrophic;
KM immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KM anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KM gene therapy; restenosis; graft versus host disease; tumour; cancer;
KM apoptotic cell death related disease; autoimmune disorder;
KM cardiovascular disorder; viral infection.

OS Homo sapiens.

PN WO200071150-A1.

XX 30-NOV-2000.

PF 18-MAY-2000; 2000WO-US13515.

PR 20-MAY-1999; 99US-0135164.

XX (HUMA-) HUMAN GENOME SCI INC.

PI Wei Y, Ruben SM, Gentz RL, Ni J;

DR WPI: 2001-041051/05.

XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PR prevention of cancer, autoimmune disorders and viral infection -

PS Disclosure: Fig 2; 285pp; English.

XX The present invention describes the human TRID protein (tumour necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumour necrosis factor
CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,
CC neurotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC activities, and can be used in gene therapy. The TRID polynucleotides
CC are useful for detecting complementary polynucleotides. TRID proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to
CC parasite, bacteria and viruses, restenosis and graft versus host disease.

CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain haematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TRID by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TRID
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis, treatment or prevention of: (a) cancer;
CC (b) autoimmune disorders; (c) diseases associated with increased
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC present sequence represents a tumour necrosis factor receptor used in
CC comparison with TRID in the exemplification of the present invention.

XX Sequence 415 AA:

Query Match 16.2%; Score 248.5; DB 22; Length 415;
Best Local Similarity 23.3%; Pred. No. 8e-10;
Matches 93; Conservative 39; Mismatches 126; Indels 141; Gaps 16;

QY 7 RUGR--GPCAAL---LLGLGLSTVTGLHCVGDTY-----PSNDRCHE 45

DB 2 rlprraspcglawgpllllgslvasgqlvppyltengtcwdqdkyyepmhdyccar 61

QY 46 CRPGNGMVRCSRQNTVCRPGCGFNDVSS-KCKRCTMCNLRSGSERKOLCTATQD 104

DB 62 cpggefvtavcarsgdtvctkcpmsynhwhlscqicrpdclvlgfevavpctsdix 121

QY 105 TVCRCRAG-----TOPIDSYKPG-----VDCAPCPGGRF--SP 135

DB 122 acrcqpgmscylldncvchceerlvlcpgyleavdeimdtvncvcpkphgnts 181

QY 136 GDNQACKPWNCTLACKHTLQPASNSDAICEDRDPAT----- 174

DB 182 sprarcqblrcelqglveaagtsydticknppegamllla11s1v1flftvta 241

QY 175 -----QPQETQGP-----ARPI-----TQPTREAWPR 197

DB 242 cawmrhpslcrklgtllkthpegeesppepadphfdleplmgsd1spspappp 301

QY 198 TS-----OGPSTRPEV---PGRAVAAIIGLGL-VIGLGLPLAILLALYLLR-- 241

DB 302 tpsleevlvlgqspdvqarelaeapgehgyavhngslhvcg--gsvevtgulylyngp 359

QY 242 -----RDQRLPPDAHKP-----PGGGSFRTPIQEE 266

DB 360 vlgtrpgpdpapppepytppeegapgselstpyed 398

RESULT 14

AAW69951
ID AAW69951 standard; Protein; 451 AA.

AC AAW69951;

DT 08-OCT-1998 (first entry)

DE RANK polypeptide partial sequence encoded by cDNA clone 9D-15C.

XX RANK; necrosis factor-kappa B; NF-KB; receptor activator; human;

KM immune response; inflammatory response; toxic shock; sepsis;

KM RANKL; RANK ligand; tumour necrosis factor; TNF.

OS Homo sapiens.

PN WO9828426-A2.

XX 02-JUL-1998.

PF 22-DEC-1997; 97WO-US23775.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059976.

```
PR 07-MAR-1997; 97US-0813509.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
XX
XX WPI; 1998-377657/32.
XX N-PSDB; AAV41375.
XX
XX New isolated ligand for receptor activator of NF-kappa B - used to
XX develop products for augmenting an immune response for inhibiting an
XX inflammatory response and for protection of cells
XX
XX Example 1; Pages 44-46; 80pp; English.
XX
XX This represents a partial sequence of the polypeptide RANK (receptor
XX activator of necrosis factor-kappab (NF-kB)). RANK is a member of
XX the tumour necrosis factor family. A soluble RANK may be used for
XX inhibiting activation of NF-kB, by contacting a cell expressing membrane
XX -associated RANK with a soluble RANK which binds to RANK ligand (RANKL).
XX RANKL polypeptides can activate RANK and can be used to induce maturation
XX of dendritic cells and enhance their allo-stimulatory capacity, thereby
XX augmenting an immune response. The soluble RANK polypeptide composition
XX may also be used for regulating an immune or inflammatory response.
XX Inhibition of NF-kB by RANK antagonists may be useful in ameliorating
XX negative effects of an inflammatory response that result from triggering
XX of RANK, e.g. in treating toxic shock or sepsis, graft-versus-host
XX reactions, or acute inflammatory reactions. They can also be used in
XX adjunct therapy for disease characterised by neoplastic cells that
XX express RANK. RANKL polypeptides can also be used to identify inhibitors
XX of RANK and thus inhibitors of an inflammatory response, and also for
XX protecting RANK-expressing cells from the negative effects of
XX chemotherapy or the presence of high levels of TNF-alpha. The products
XX can also be used for detection and drug screening.
XX
XX Sequence 451 AA:
SQ
Query Match 16.1%; Score 247; DB 19; Length 451;
Best Local Similarity 33.3%; Pred. No. 1.1e-09;
Matches 70; Conservative 21; Mismatches 83; Indels 36; Gaps 10;
QY 1 MCVGARRLGRCPCALLLL-----GLGLSTVYGLHCVGDY-YPNDRCHECRPGNGMS 54
DB 1 maparr--rrplfallllcallarlgvalqiapptsekhyehlgrcnkccepgkyms 58
QY 55 RCSRSONTVCRPGCGPFYNDVSSK-PCKPCTWNL-----RSGSERKQLCTA-- 101
DB 59 kcttsdsavclpcgpdelyldsmneedkcllhkvcdtgtkalaavvagnstpractag 118
QY 102 --TODTVRCRCRAGTQ-----PLDSYKPGVDCAPCPGFHSP--GDNOACKPWTNCT 148
DB 119 hwsqdeec-crrntecapjgaghpqlnkdtv-ckpelagysfdaafstckcpwtinct 176
QY 149 LAGKHTLQPASNSSDAICEDRDPATQPOE 178
DB 177 flgkrvehgltksdavcsslparkpne 206
RESULT 15
AAW68287
ID AAW68287 standard; Protein; 451 AA.
AC AAW68287;
XX
XX 08-OCT-1998 (first entry)
XX
XX RANK polypeptide partial sequence encoded by cDNA clone 9D-15C.
XX
XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
XX immune response; inflammatory response; toxic shock; sepsis;
XX RANKL; RANK ligand; tumour necrosis factor; TNF.
XX
```

```
OS Homo sapiens.
XX
XX W092828424-A2.
XX
XX 02-JUL-1998.
XX
XX 22-DEC-1997; 97MO-US23866.
XX
XX 14-OCT-1997; 97US-0064671.
XX 23-DEC-1996; 96US-0059978.
XX 07-MAR-1997; 97US-0813509.
XX
XX (IMMV ) IMMUNEX CORP.
XX
XX Anderson DM, Galibert LJ, Maraskovsky E;
XX
XX WPI; 1998-377655/32.
XX N-PSDB; AAV41369.
XX
XX New isolated receptor activator of necrosis factor-kappa B - useful
XX for, e.g. developing products for regulating an immune or
XX inflammatory response, treating toxic shock or sepsis
XX
XX Example 1; Pages 44-46; 80pp; English.
XX
XX This represents a partial sequence of the polypeptide RANK (receptor
XX activator of necrosis factor-kappab (NF-kB)). RANK is a member of
XX the tumour necrosis factor family. Host cells transformed or transfected
XX with an expression vector comprising the RANK encoding nucleic acid can
XX be used to produce recombinant RANK protein. The soluble RANK may be used
XX for inhibiting activation of NF-kB, by contacting a cell expressing
XX membrane-associated RANK with a soluble RANK which binds to RANK ligand
XX (RANKL). The soluble RANK polypeptide composition may also be used for
XX regulating an immune or inflammatory response. Inhibition of NF-kB by
XX RANK antagonists may be useful in ameliorating negative effects of an
XX inflammatory response that result from triggering of RANK, e.g. in
XX treating toxic shock or sepsis, graft-versus-host reactions, or acute
XX inflammatory reactions. They can also be used in adjunct therapy for
XX disease characterised by neoplastic cells that express RANK. The products
XX can also be used for detection and drug screening.
XX
XX Sequence 451 AA:
SQ
Query Match 16.1%; Score 247; DB 19; Length 451;
Best Local Similarity 33.3%; Pred. No. 1.1e-09;
Matches 70; Conservative 21; Mismatches 83; Indels 36; Gaps 10;
QY 1 MCVGARRLGRCPCALLLL-----GLGLSTVYGLHCVGDY-YPNDRCHECRPGNGMS 54
DB 1 maparr--rrplfallllcallarlgvalqiapptsekhyehlgrcnkccepgkyms 58
QY 55 RCSRSONTVCRPGCGPFYNDVSSK-PCKPCTWNL-----RSGSERKQLCTA-- 101
DB 59 kcttsdsavclpcgpdelyldsmneedkcllhkvcdtgtkalaavvagnstpractag 118
QY 102 --TODTVRCRCRAGTQ-----PLDSYKPGVDCAPCPGFHSP--GDNOACKPWTNCT 148
DB 119 hwsqdeec-crrntecapjgaghpqlnkdtv-ckpelagysfdaafstckcpwtinct 176
QY 149 LAGKHTLQPASNSSDAICEDRDPATQPOE 178
DB 177 flgkrvehgltksdavcsslparkpne 206
```

Search completed: June 18, 2002, 14:25:20
Job time: 84 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 14:34:42 ; Search time 2703.24 Seconds
(without alignments)
8190.274 Million cell updates/sec

Title: US-09-852-845-1
Perfect score: 1058
Sequence: 1 cagcagagcagcagatgtgc.....cacaataaacccttgccag 1058

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:*

1: gb_pa:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sy:*
12: gb_un:*
13: gb_vi:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sy:*
28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
------------	-------------	-------	--------	-------	-------------

1	1044.4	98.7	1057	6	AR048669	AR048669 Sequence
2	1044.4	98.7	1057	6	AR156875	AR156875 Sequence
3	1016.2	96.0	1034	9	S76792	S76792 OX40-cell s
4	888.2	84.0	1373	4	HSBOX40MR	X75962 H. sapiens m
5	472.6	44.7	877	4	AB003911	AB003911 Rabbit mr
6	389.8	36.8	210944	2	AL162741	AL162741 Homo sapi
7	388.2	36.7	5150	9	AL390719	AL390719 Homo sapi
8	375.6	35.5	1017	10	HSAT277151	AJ727751 Homo sapi
9	375.6	35.3	883	10	RSOX40	X17037 Rat mRNA fo
10	373	35.3	883	10	MMOX40	221674 M.musculus
11	286.6	27.1	1317	6	AR019521	AR019521 Sequence
12	286.6	27.1	1317	6	IL4936	IL4936 Sequence 10
13	283.2	26.8	618	6	AR019518	AR019518 Sequence
14	283.2	26.8	618	6	IL4933	IL4933 Sequence 6
15	124.4	11.8	6080	6	AX251336	AX251336 Sequence
16	111.2	10.5	117	6	AX134865	AX134865 Sequence
17	111.2	10.5	117	6	AX134963	AX134963 Sequence
18	111.2	10.5	117	6	AX135076	AX135076 Sequence
19	109.4	10.3	117	6	AX134865	AX134865 Sequence
20	109.4	10.3	117	6	AX134962	AX134962 Sequence
21	109.4	10.3	117	6	AX135075	AX135075 Sequence
22	108.8	10.3	6080	6	AX251335	AX251335 Sequence
23	103.4	9.8	2907	10	MMDNROX40	X85214 M.musculus
24	103.4	9.8	60953	2	AC100470	AC100470 Mus muscu
25	103.4	9.8	99098	2	AC095793	AC095793 Rattus no
26	103.4	9.8	253111	2	AL627204	AL627204 Mus muscu
27	103.4	9.8	254197	2	AF389853	AF389853 Mus muscu
28	101.6	9.6	5148	6	AX251339	AX251339 Sequence
29	79.8	7.5	5148	6	AX251340	AX251340 Sequence
30	68.6	6.6	125020	9	AF429315	AF429315 Homo sapi
31	68.2	6.0	523520	9	AF429315	AF429315 Homo sapi
32	63.4	6.0	523520	2	AC010772	AC010772 Homo sapi
33	62	5.9	197669	2	AC084064	AC084064 Homo sapi
34	61	5.8	65898	2	AC090435	AC090435 Chlamydom
35	61	5.8	100006	2	AC090436	AC090436 Chlamydom
36	60.8	5.7	63629	2	AC091187	AC091187 Homo sapi
37	59.2	5.6	303091	2	AC084799	AC084799 Mus muscu
38	57	5.4	161307	2	AC084058	AC084058 Homo sapi
39	56.8	5.4	113056	2	AC102988	AC102988 Rattus no
40	56.2	5.3	224923	2	AC068947	AC068947 Mus muscu
41	56	5.3	705	9	AF117297	AF117297 Homo sapi
42	56	5.3	723	6	AX074382	AX074382 Sequence
43	56	5.3	726	6	AF125304	AF125304 Homo sapi
44	56	5.3	1006	9	AR108738	AR108738 Sequence
45	56	5.3	1008	6	AX055408	AX055408 Sequence

ALIGNMENTS

RESULT 1.

LOCUS AR048669 1057 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 1 from patent US 5821332.

ACCESSION AR048669

VERSION AR048669.1 GI:5971012

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1057)

AUTHORS Godfrey,W., Buck,D. and Engleman,E.G.

TITLE Receptor on the surface of activated CD4.sup.+ T-cells: ACT-4

JOURNAL Patent: US 5821332-A 1 13-0CT-1998;

FEATURES

source location/Qualifiers

1..1057

BASE COUNT 176 a 390 c 344 g 147 t

ORIGIN

Query Match 98.7%; Score 1044.4; DB 6; Length 1057;
Best Local Similarity 99.8%; Pred. No. 1.1e-150;

Matches 1056: Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
OY 1 cagcagagacgaagatgtgctgctgggagctcggcggctgggacggcgctgtgcgctc 60
    |||||||
Db 1 CAGCAGAGACGAGATGTGCTGGGGGCTCGGCGGCTGGGCGGCGGCTGTGCGGCTC 60
OY 61 tgcctcctcctggcctggcctggcctggcctggcctggcctggcctggcctggcctgg 120
    |||||||
Db 61 TGCCTCCTCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 120
OY 121 acccagacgaacgaacggctgtcgcacgaatgcagacgaacgaacgaacgaacggct 180
    |||||||
Db 121 ACCCAGACGACGACGCGTGTCTGCCAGAGTGCAGGCGCAGGCAAGGAGTGTGACCGCT 180
OY 181 gcaagcgcctccagaaacagctgtgcgctcgtgcgagcgcggtgtctctcaagacgttg 240
    |||||||
Db 181 GCAGCGCGCTCCAGAAACAGGCTGCTCCGCTCGCGGCGGCGGCTCTCAACAGACGTGG 240
OY 241 tcaagctcaagcgcgtgcagacgctgcagctgtgttaactcaagaagtggagtgagcgga 300
    |||||||
Db 241 TCAGCTCCAGCGCGTGCAGGCCCTCGACGCTGGTGAACCTCAGAAGTGGAGTGAAGCGGA 300
OY 301 agcagcgtgtcagcgcgcacacagacagacagctgtgcgctgtgcgagcgagccagcccc 360
    |||||||
Db 301 AGCAGCTGTGCAGCGGCGCACACAGACAGACAGTGTGCGCGCTGCGGCGGCGGCGCACCGCC 360
OY 361 tggagacgtcaaacgctgtgagttgactgtgcgctgtgcgctgtgcgctgtgcgctgtgc 420
    |||||||
Db 361 TGGACAGCTACAAAGCCTGGAGCTTGACTGTGCTGCGGCGGCGGCTCTCAAGGCGCTTCCCGCC 420
OY 421 gggaaacacagcgctgcagacgctgtgaacacttgacactgtgtggagacacacgtgc 480
    |||||||
Db 421 GGGAAACACAGGCGCTGCAGGCCCTGTGACCACTGTGCTGTGGAGACACACCGCTTC 480
OY 481 agcgcgcagcaataagctcgcagacgaatctgtgagaaacagagacacccagacagcgagc 540
    |||||||
Db 481 AGCGCGCAGCAATAAGCTCGAGACGAATCTGTAGAGACAGGAGACCGCCAGCGCACGAGAC 540
OY 541 cccagagaaacacagggcccccccgccagggcccaactgtctcagacgaactgaagcctgagc 600
    |||||||
Db 541 CCCAGAGAACCCAGGGCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
OY 601 ccaagacactcaagagacacccctcaccccgccgtggaagctcccgaggcgctgtgcgttg 660
    |||||||
Db 601 CCAGAACTCAAGAGGACCTTCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
OY 661 ccgcacactcctggcctgtgcgtgtgcgtgtgcgtgtgcgtgtgcgtgtgcgtgtgcgtgtg 720
    |||||||
Db 661 CCGCATCTCGGCGCTGGGCGCTGTGCTGGGCGCTGTGCGGCGGCGGCGGCGGCGGCGGCGG 720
OY 721 cccgttaactcgtctcggaggaggacgaagcctgtcccccgatgtcccaaaagccccctgggg 780
    |||||||
Db 721 CCTTACTCTGCTCGGAGGAGACAGAGGCTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
OY 781 gagcagcttccagagaccccatcgaagagagcagccgaagcccaactcgaactcggagca 840
    |||||||
Db 781 GAGCAGCTTCCGAGACCCCATCAAGAGAGCAGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
OY 841 agatctgaacttggcccaacgaagtgtgacgtgtggcccgccagcgtgtgaagcccgagag 900
    |||||||
Db 841 AGATCTGACG-TGGGCGCACCAAGGTGAGCGCTGGGCGGCGGCGGCGGCGGCGGCGGCGG 899
OY 901 gctcgtcgtggagagcaggtgtgcaggtgcgctgtgcgagcgacgtctcgtggcgaact 960
    |||||||
Db 901 GTCTGTCTGGGCGAGAGGCGAGGTGACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 959
OY 961 ctgcacgcgttctcaggtgcagatgtgcctcgcgctgtcctgtcttcaatgtcagatga 1020
    |||||||
Db 960 CTGCACCGCTTCTAGGTGCGGATGCGCTCGGCGCTCTCTGCTTACGATGCGCATGCAATA 1019
OY 1021 cctcctgcgcgcgcggagacacaataaaacacttggcag 1058
    |||||||
Db 1020 CCTCTGCGCGGCGGAGCACCAATAAAACCTTGGCAG 1057
```

```
RESULT 2
AR156875 1057 bp DNA linear PAT 08-AUG-2001
LOCUS AR156875
DEFINITION Sequence 1 from patent US 6242566.
ACCESSION AR156875
VERSION AR156875.1 GI:15125579
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1057)
AUTHORS Godfrey,W. and Engleman,E.G.
TITLE Ligand (ACT-4-L) to a receptor on the surface of activated CD4+
T-cells
JOURNAL Patent: US 6242566-A 1 05-JUN-2001;
FEATURES
source
BASE COUNT 176 a 390 c 344 g 147 t
ORIGIN
```

Query Match 98.7%; Score 1044.4; DB 6; Length 1057;

Best Local Similarity 99.8%; Pred. No. 1,1e-150; Matches 1056; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

```
OY 1 cagcagagacgaagatgtgctgctgggagctcggcggctgggacggcgctgtgcgctc 60
    |||||||
Db 1 CAGCAGAGACGAGATGTGCTGGGGGCTCGGCGGCTGGGCGGCTGTGCGGCTC 60
OY 61 tgcctcctcctggcctggcctggcctggcctggcctggcctggcctggcctggcctgg 120
    |||||||
Db 61 TGCCTCCTCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 120
OY 121 acccagacgaacgaacggctgtcgcacgaatgcagacgaacgaacgaacgaacggct 180
    |||||||
Db 121 ACCCAGACGACGACGCGTGTCTGCCAGAGTGCAGGCGCAGGCAAGGAGTGTGACCGCT 180
OY 181 gcaagcgcctccagaaacagctgtgcgctcgtgcgagcggtgtctctcaagacgttg 240
    |||||||
Db 181 GCAGCGCGCTCCAGAAACAGGCTGCTCCGCTCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
OY 241 tcaagctcaagcgcgtgcagacgctgtgacactgtgttaactcaagaagtggagtgagcgga 300
    |||||||
Db 241 TCAGCTCCAAAGCGGTGCAGGCCCTGTGACTGTGTGAACCTCAGAAGTGGAGTGAAGCGGA 300
OY 301 agcagcgtgtcagcgcgcacacagacagacagctgtgcgctgtgcgagcgagccagcccc 360
    |||||||
Db 301 AGCAGCTGTGCAGCGGCGCACACAGACAGACAGTGTGCGGCGGCGGCGGCGGCGGCGGCGG 360
OY 361 tggagacgtcaaacgctgtgagttgactgtgcgctgtgcgctgtgcgctgtgcgctgtgc 420
    |||||||
Db 361 TGGACAGCTACAAAGCCTGGAGTTGACTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
OY 421 ggcacaacacagggcctgcagacgctgtgaacactgtcaacttgccttggagaaacacccct 480
    |||||||
Db 421 GGCACAACACAGGCGCTGCAGGCCCTGTGACCACTGTGCTGTGGAGAGCACACCGCTTC 480
OY 481 agcgcgcagcaataagctcgcagacgaatctgtgagaaacagagacaccccgagcgaagc 540
    |||||||
Db 481 AGCGCGCAGCAATAAGCTCGAGCGCAATGTGAGAGACAGGAGACCGCCCGAGCGACGACAC 540
OY 541 cccagagaaacacagggcccccccgccagggcccaactcactgttccagccactgaagcctggc 600
    |||||||
Db 541 CCCAGAGAACCCAGGGCCCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 600
OY 601 ccaagacactcaagagacacccctcaccccgccgtggaagctcccgaggcgctgtgcgttg 660
    |||||||
Db 601 CCAGAACTCAAGAGGACCTTCACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
OY 661 ccgcacactcctggcctgtgcgtgtgcgtgtgcgtgtgcgtgtgcgtgtgcgtgtgcgtgtg 720
```

	Db	661	CCGCATCTTGGGCTTGAGCCTGTGGTCTGGGCTGTCTGTGGCCCCCTGGCATTCCTGTGCG	720
Oy	721	ccttgtaacctgctccgaagagaccagaagctgtccccccatgatgcacaaagccccttggag	780	
Db	721	CCCTGTACTCTGCTCCGAGGAGACAGAGAGCTGCCCCCAGTAGCCCAAGAGCCCCCTGGGG	780	
Oy	781	gaggcagtcttcggagaccccccatccaagagagcgacggccgaagcccaatccaatctgacga	840	
Db	781	GAGGAGATTCTCCGAGACCCCATCACAAAGAGAGAGAGGCGAGGCCACATCCACTCTGGGCA	840	
Oy	841	agatctgaccttgtagcccaagaagtgaagctgtgcccgcgcacaagctgtgagcccgagag	900	
Db	841	AGATGTGACC-TGGGCCCCAACAGAGTTGAAGCTGGGCCCCGCCAAGGTGAGAGCCGAGAG	899	
Oy	901	gtctgtctggcgaagcagcagcagctgtcagcgcctgtccgcgcacagctctgtggccaact	960	
Db	900	GTCTGTCTGGGCGAGAGGAGGTCAGGCGCCGCTGCGCCGCCACAGGCTCTGTGGGCAACT	959	
Oy	961	ctgcaacgcttcaagtgtgcagatgtgctgtccgcgcctctcattcaatgatacatgata	1020	
Db	960	CTGCACCGTTCTAGGTGCGCGATGCTGCTCCGCGCTCTCTGCTTAAGTATGCATGATA	1019	
Oy	1021	cctctgtcccgcgagaccacaataaaaaaccttggcag	1058	
Db	1020	CCTCTGCCCCGCGGAGCACATTAATAAACTTGGCAG	1057	
RESULT	3			
LOCUS	S76792	1034 bp	mRNA	linear PRI 02-JUN-2000
DEFINITION	OX40-cell surface antigen [human, mRNA Partial, 1034 nt].			
ACCESSION	S76792			
VERSION	S76792.1	GI:913405		
KEYWORDS				
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 1034)			
AUTHORS	Baum P.R., Gayle R.B.III., Ramsdell F., Srinivasan S., Grabschein K., Alderson M.R. et al.			
TITLE	Identification of OX40 ligand and preliminary characterization of its activities on OX40 receptor			
JOURNAL MEDLINE	Circ. Shock 44 (1), 30-34 (1994)			
REMARK	95219871			
FEATURES	GenBank staff at the National Library of Medicine created this entry [NCBI g1dbsq 163567] from the original journal article. This sequence comes from Fig. 3A.			
source	Location/Qualifiers			
	1..1034			
gene	/organism="Homo sapiens"			
	/db_xref="taxon:9606"			
	<1..1034			
	/gene="OX40"			
	<1..825			
	/gene="OX40"			
	/note="cell surface antigen; This sequence comes from Fig. 3A"			
	/codon_start=1			
	/product="OX40"			
	/protein_id="AAB33944.1"			
	/db_xref="gi:913406"			
	/translation="LARRLRGPCAALLLLGLSTVYTLHCVCSDVPSPNDRCHBERPGNMVSRCSRSQNTWCPGPGFYNDIVSSKPKPCMCNLRSGBRKOCTADTDPTVCRBAGTQPLDYSKPGVDCAKCPGHFSPGDNAOKPMWTCLAGHTLTLOPASNSDDACIDRDPAPOEOTGCPARAPRTLYTOTPEAMPTSGSPSTRPVEVGGRAYVAIILDLGLVLGLPAILALTYLTRKDQLRPDAHKRPDGGSFTPTIQEDAHASTLAKT"			
CDS				
BASE COUNT	169 a 386 c 333 g 146 t			
ORIGIN				

[illegible]

```

|||||
Db 1022 AAAACCTTGCGAG 1034

RESULT 4
LOCUS HSHOX40MR 1373 bp mRNA linear PRI 13-MAY-1994
DEFINITION H.sapiens mRNA for OX40 homologue.
ACCESSION X75962
VERSION X75962.1 GI:472957
KEYWORDS OX40 antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1358)
AUTHORS Latza,U., Durkop,H., Schmittiger,S., Ringeling,J., Eitelbach,F.,
Hummel,M., Fomatsch,C. and Stein,H.
The human OX40 homologue: cDNA structure, expression and chromosomal
assignment of the ACT35 antigen
Eur. J. Immunol. 24 (3), 677-683 (1994)
94170844
JOURNAL 2 (bases 1 to 1373)
MEDLINE Latza,U.
REFERENCE Direct Submission
AUTHORS Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz,
JOURNAL Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG
FEATURES
source Location/Qualifiers
1..1373
/organism="Homo sapiens"
/db_xref="taxon:9606"
6..839
/codon_start=1
/product="OX40 homologue"
/protein_id="CAA5376.1"
/db_xref="GI:472958"
/db_xref="SWISS-PROT:P43489"
/translation="MVGARRLRGSPCAALLIGLSTVTGLHGVDPYSPNDRCCH
ECRBNQNVSRCSRSQNTVCRCRGFPNDVYSSRPCKPTMCNLRSSSEKQDCTAT
QDTVCRKAGTQPLDSYKPGVDACAPRGHSPGNQCKPNTCTLGGKHLQPSN
SSDAICEDRDPRATQPEQTGPPAPRTIVQTEAMPRTSOGSTRPVPGRAVAAI
LGLGLVGLGLPLALILALYLRLRDQRLRPRAHKPRGSGSFRTIOEBQADAHSTLAK
I"
sig_peptide 6..89
mat_peptide 90..836
repeat_region 814..958
repeat_region 959..1079
polya_signal 1341..1346
polya_site 1358
BASE COUNT 257 a 452 c 423 g 241 t
ORIGIN
Query Match 84.0%; Score 888.2; DB 9; Length 1373;
Best Local Similarity 99.6%; Pred. No. 8.3e-127;
Matches 901; Conservative 0; Mismatches 3; Indels 1; Gaps 1;

```

```

Oy 250 agccgtgcaagccctgcaagtgtagtgaacctcagaagtggagtgagcggaagcaagctgt 309
|||||
Db 241 AGCCGTGCAAGCCCTGCACGTGGTGAACCTCAGAAGTGGAGTGAAGCGGAACACACTGT 300
Oy 310 gcaagcgcaacagagacacagtcgtccgtctgcggcgccggaaccccgcccttgaaagct 369
|||||
Db 301 GCACGGCCACACAGACACAGTCTGCGCTGCCGGCGGGCCAGCCACCGCTTGACAGCT 360
Oy 370 acaagcctgagtgatctgtgccccctgcctcacaaggaactctctcccaagcgacaacc 429
|||||
Db 361 ACAAGCCTGAGATGTGACTGTGCCCCCTGCTCCAGGGCACTTCTCCAGGGAGAAC 420
Oy 430 aggcctgcaagccctggaacaaactgcaacttgctgctgggaagacacccctgcaagcgca 489
|||||
Db 421 AGGCCTGCAAGCCCTGACCACTGACCACTGCTGGTGGGAAGCACACCTGCACCCGCCCA 480
Oy 490 ggaatgctcgagagcaatctgtgagaagaagagagagagagagagagagagagagaga 549
|||||
Db 481 GCAATAGCTCGAGCAATCTGTGAGACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Oy 550 cccaagggcccccggcgaagggcccatcactgtccagcccaactggaagcctggcccaagact 609
|||||
Db 541 CCCAGGGCCCCCGGCGCAGAGCCCATCATGTCACAGCCCATGAAGCCTGGCCAGAACCT 600
Oy 610 caaaggaaccttcacacgcggcgtggaaggtcccgaggcgctgcgtgctgcgcacatcc 669
|||||
Db 601 CACAGGAGACCTTCACACCGCCCGTGAAGGTCCCGGGGGCGCTGGGTGGCCCATCC 660
Oy 670 tgggcctgggacctgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 729
|||||
Db 661 TGGGCTGGGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Oy 730 tgcctcggaggagaccagagctgtcccccgatgagcccaagagcccttgaggagagagct 789
|||||
Db 721 TGCCTCGGAGGAGGACAGAGGCTCCCGCCGATGCCCAAGAGCCCTGGGGGAGGAGCT 780
Oy 790 tcggagccccctcagaaggagagagagagagagagagagagagagagagagagagagag 849
|||||
Db 781 TCCGGACCCCATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGATGTGAC 840
Oy 850 ctggagcccaacaggtgagcgtgagcccgccgaagcctggaagcccgagagctgtctgtg 909
|||||
Db 841 C-TGGGCCACCAAGGTGAGAGCTGGGCCCGCCGACAGCTGGAGCCGGAGGGGTCTGTGG 899
Oy 910 gcgag 914
Db 900 GCGGG 904

RESULT 5
AB003911 877 bp mRNA linear MAM 05-FEB-1999
LOCUS Rabbit mRNA for OX40 precursor, partial cds.
DEFINITION AB003911
ACCESSION AB003911.1 GI:2114107
VERSION OX40
KEYWORDS Oryctolagus cuniculus (sub-species:domesticus, strain:Chbb:HW)
SOURCE HTLV-I-transformed T cell line:H446 cDNA to mRNA.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 877)
AUTHORS Isono,T.
JOURNAL Submitted (14-MAY-1997) Takahiro Isono, Shiga University of Medical
Science, Central Research Laboratory, Seta Tsukinowachou, Otsu,
Shiga 520-2192, Japan (E-mail:isono@elle.shiga-med.ac.jp,
Tel:81-775-48-2308, Fax:81-775-48-2048)
2 (sites)
REFERENCE Isono,T. and Seto,A.
AUTHORS Expression of OX40 and OX40 ligand genes in rabbit
JOURNAL HTLV-I-transformed T cell lines

```

JOURNAL FEATURES	Unpublished (1997)
source	location/Qualifiers 1..877
	/organism="Oryctolagus cuniculus" /strain="Chdb:HM" /sub_species="domesticus" /db_xref="taxon:9986" /cell_line="H46" /cell_type="HLV-I-transformed T cell"
sig_peptide	<1..54
CDS	<1..804 /codon_start=1 /product="Ox40 precursor" /protein_id="PAA20059.1" /db_xref="GI:2114108" /translation="GLAALGALLLLGLLGAAPRPDVEDYTPGDRCLEQEPYGMVSRCHNSODTICHPCPEGFYNFAVYIAOKPCITOCNRSSEPDCEHTRTVERCRPTSTPLNGKRGVDCAPCPOGHFSGNNRACPMWNTLAGRLTOPASSISDAVCEDRSIATOPWEPTSPASRYREPRTASTSWAMPYTAGPSTPLEASKPOLIVSLGIGLGILALLAAILALTYLHORAWMPKLPGGSFRPIIOEQADAGSMAKI"
mat_peptide	55..801 /product="Ox40"
BASE COUNT	157 a 324 c 275 g 121 t
ORIGIN	
Query Match	44.7%; Score 472.6; DB 4; Length 877;
Best Local Similarity	72.6%; Pred. No. 3.4e-63;
Matches 644; Conservative	0; Mismatches 229; Indels 14; Gaps 2;
Oy	34 ggcgtggcgcgagcggtgtgcggtctgtctctctcttgaggcttggagtgaacacctga 93
Db	2 gccctggccgcagcgtccggctttggcccttcgtctcctcgtcggtcctcgtgggtctgagc 61
Oy	94 cgaggctcacactgttgtgggagaccattcccagaagaacgcgtgtgcgtccaagatga 153
Db	62 ccagcccgagactgccctttggggagaccttaccctccggcggaacggatgcttggatgcc 121
Oy	154 ggcacagcaagcggtgtgtagcgcttgacgcgtccacgaagaacggtgtgtgctccgt 213
Db	122 agccagcgctacggcatggtgagccctcgttaaacgcagcacagacacatctgccaccgt 181
Oy	214 gcgggcgcgggtcttacaagaacgctgtgtcaggtccaagcgtgtgaagcccttgaaagt 273
Db	182 gggaaccccgctttacaaacgaagctgtcaattaccaaacctgtcaaacgcttgacaagt 241
Oy	274 gtaacctcaagaagtgtggagttagcggaagcaactgttgacgycgcaacaagaacagct 333
Db	242 gcatacagagaagagcggaagtgaacccacagacgaagtgcacccacacagacacacgtct 301
Oy	334 gcgcgttcgcggcggtgcaaccagcccccttgagcagttacaagcttgaagtgtgtccc 393
Db	302 gccgctggccggccagacacccagcccttgaaacggcttacaaagcagcagagtgactgtgcc 361
Oy	394 ccttgcccttcagagactcttctccagagagaaacagagcgtgcgaagcccttgagcaact 453
Db	362 cctggccccagggccacttctccgagggcaaaacccggccttgcaagcccttgaccact 421
Oy	454 gaaccttggcttgaagcacaccttgcagccggcagcagacatatgtctcogaagcaactgtg 513
Db	422 gcaccttaccttggaaagcggaactgacacccggcagcagcattctcgacgctgtgtctgg 481
Oy	514 aggaacaggaacccccagcacacgcagccccagagagaacccagagccccccagagccca 573
Db	482 aggaacaggaagctccctggccacacaccccttggaagaccccccagtccttaccggcccc 541
Oy	574 tcacttctcagcccaacttgaaccttgccccagagaacacacagagacaccttcaaccggcccc 633
Db	542 ccacggccacgaacttccaaagcctggccccagagacacacccagggctccttccacaccacct 601
Oy	634 ttgaagttcccgaggcgctgtcgtgttcgcacatcttgagcttggccttggctgtgtcgggc 693
Db	602 ttgagagccttccaaagggccccccagcttggcccttatgtcttggaccttggcccttggccgc 661

QY	654	ttgtggggcccccttggaactctctgtgagccctgactcgtctccgaaggagaccagagctgc	753
Db	662	TGCTGGCCCTCTGGCTGCTGCTGCTGGCCCTGTACTCTGCACCAAGAGGCGCTGGAGGC	718
QY	754	ccccgacgcacaaagccccctgtgggagggacgatttcgcgaccgcccaataagaagagc	813
Db	719	-----CCCCAAGCTCCTTGAGAGGAGGAGACGTTCCGAGACCCCATTCAGAGAGAGC	769
QY	814	agggcgcagcccaactcaccctcgtggccaagatctgaccttggcccccaaggtgagcgt	873
Db	770	AGGCAAGATGCTGGTTCCACATGCGCAAGATCTAGC--ACCATTCGCCGCGAGGGGCT	827
QY	874	ggggcccgccagagctgtagagcccgagggtctgcgtgggagacagggc	920
Db	828	GCATCACCACAGGCTGGCCCTCGGGGGTAGGGGGCCAGGACGAGGC	874
RESULT	6		
LOCUS	AL162741/c		
DEFINITION	AL162741	111119 bp	DNA linear HTG 08-FEB-2002
ACCESSION	AL162741		
VERSION	AL162741.24	GI:18643745	
KEYWORDS	HTG: HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (sites)		
JOURNAL	Harrison, E.		
COMMENT	Direct Submission		
	Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,		
	Cambridgeshire, CB10 1SA, UK. E-mail enquiries:		
	humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk		
	On Feb 10, 2002 this sequence version replaced gi:18642353.		
	----- Genome Center		
	Center: Wellcome Trust Sanger Institute		
	Center code: SC		
	Web site: http://www.sanger.ac.uk		
	Contact: humquerry@sanger.ac.uk		
	----- Project Information		
	Center project name: dj902P8		
	----- Summary Statistics		
	Assembly program: XGAP4; Version 4.5		
	Sequencing vector: Plasmid; L08752; 100% of reads		
	Chemistry: Dye-terminator ET-amersham; 16% of reads Chemistry:		
	Dye-terminator Big Dye; 83% of reads		
	Consensus quality: 110490 bases at least Q40		
	Consensus quality: 110677 bases at least Q30		
	Consensus quality: 110755 bases at least Q20		
	Insert size: 110819; sum-of-ctgts		
	Insert size: 160089; 6.7% error; agarose-fp		
	Quality coverage: 8.36x in Q20 bases; sum-of-ctgts Quality		
	coverage: 5.95x in Q20 bases; agarose-fp		

	* NOTE: This is a 'working draft' sequence. It currently		
	* consists of 4 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
	* 1 42985: contig of 42985 bp in length		
	* 42986 43085: gap of 100 bp		
	* 43086 54937: contig of 11852 bp in length		
	* 54938 55037: gap of 100 bp		
	* 55038 67254: contig of 12217 bp in length		
	* 67255 67354: gap of 100 bp		
	* 67355 111119: contig of 43765 bp in length.		
FEATURES	Location/Qualifiers		

```

source
1..11119
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP5-902P8"
/clone_1lb="RPC1-5"
1..42985
/note="assembly_fragment:00240
fragment_chain:1
clone_end:SP6
vector_side:left"
43086..54937
/note="assembly_fragment:02853
fragment_chain:1"
55038..67254
/note="assembly_fragment:00075
fragment_chain:1"
67355..11119
/note="assembly_fragment:02810
fragment_chain:1"

BASE COUNT      22049 a  35882 c  32333 g  20555 t    300 others
ORIGIN

```

Query Match	36.8%	Score 389.8	DB 2	Length 111119
Best Local Similarity	76.2%	Pred. NO. 4.5e-51		
Matches 609	Conservative 0	Mismatches 2	Indels 188	Gaps 3
QY 447	accacaatgacaccttgcctgtggaagacacacacccctgtcacagccggtccgaagcaatagctcgtgacgca			506
Db 22255	AACAGCTGACACCTTGCTGGTGGAGAACACACCTGACAGCCGGCCAGCAATATGCTGGAGCGCA			22196
QY 507	atctgtgtgagacagggagacccccagacacgacagcccaaggagagaccacagggccccccgagcc			566
Db 22195	ATCTGTGAGGACAGAGGACCCCCACACGCAAGCCCCAGGAACCCAGGGCCCCCGGGCC			22136
QY 567	aggccacacactgtctcagaccacatgaaagccttgcgcccagaaccttcacagagacccctccacc			626
Db 22135	AGGCCCATCTACTGTCTCAACCCCACTGAACCTTGCCCCAGAACCTCACAGGGACCTTCACCC			22076
QY 627	cgagccgctgtagagtgctccggggg-----			647
Db 22075	CGGCCCGTGGAGATCCCCGGGGGTAAAGGGCGCCTGGCCAGCCCAAGGGGGCCCCCAACC			22016
QY 648	-----			647
Db 22015	CGAATAGGAGAAAGGGAGAGGGGCGCATGGGGGCCCTCCTGTGGACCCACCCAGCAGACC			21956
QY 648	-----ggcgctgaggttgcgcgacatccttgagcccttgagccctgagcgtgagcttgagctgct			697
Db 21955	CCCTTCCTGACAGGCGGTGGGTGGCGCCATCTCGGGCCCTGGGGCTGTGCTGTGGGCTGCT			21896
QY 698	gggcgcctctgacatcctctgcctgtacactgtctcgcgaagagacgaagctgacccc			757
Db 21895	GGGCCCCCTGGCCATCTGCTGTGGCCCTTACTGCTGCTCGGAGAGACACAGAGCTGCCCC			21836
QY 758	cgatgtgccacaagccccct-----			776
Db 21835	CGATGCCCCAACAGCCCTCTGTGATGCTCATGAGCCTTGCCGCACATGCTCTGCGGGT			21776
QY 777	-----ggggagagcagtttcggaaccc			799
Db 21775	GAGGCCCAACCCACCATCTCTCTTTTTCCTTCCCAAGAGGGGAGGACAGTTTCCGAGCC			21716
QY 800	catccaagagagagcagcgcgagacccacttcaacccttgaccgaagatctagacttggaccaca			859
Db 21715	CATCCAAAGAGAGCAGGCGCCGAGCGCCACTCCACCTTGCGCCAAAGATCTGACC-TGGGCCCA			21657
QY 860	ccaaggtggaagccttggcccgcgacagagcttggaagcccgagaggttctgtcttggcgacagag			919
Db 21656	CCAAGGTGAGAGCTGTGGGCCCGCCGACAGGCTGGAGCCCGGAGGGGTCTGTGTGGCGAGACAGGG			21597
QY 920	caggtgcaagcgcgcctgcgccgcgacagctccttgcgcaacttgcacgcttctagtgtgcc			979

QY	980	gatggctgccttcggctctctgcttaagtaagtaagcataactcttcgccccgcggagacc	1039
Db	21536	GATGGCTGCTCTCGGCTCTGCTTAAGTAAGCATAACTCTCTCCCGCGGAGACC	21477
QY	1040	acaataaaaccttgcgcag	1058
Db	21476	ACAATAAAACCTTGCAG	21458
RESULT	7		
AL390719			
LOCUS			
DEFINITION	AL390719	210944 bp	DNA
ACCESSION	AL390719		Linear
VERSION	AL390719.25	GI:18476612	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
TITLE	McLay, K.		
JOURNAL	Direct Submission		
COMMENT	Submitted (24-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerys@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Feb 1, 2002 this sequence version replaced g1:16304463.		
	----- Genome Center		
	Center: Wellcome Trust Sanger Institute		
	Center code: SC		
	Web site: http://www.sanger.ac.uk		
	Contact: humquerys@sanger.ac.uk		
	----- Project Information		
	Center project name: B465B22		
	----- Summary Statistics		
	Assembly program: XGAP; version 4.5		
	Sequencing vector: plasmid; L08752; 100% of reads		
	Chemistry: Dye-terminator ET-amersham; 2% of reads		
	Dye-terminator Big Dye; 97% of reads		
	Consensus quality: 201072 bases at least Q40		
	Consensus quality: 204266 bases at least Q30		
	Consensus quality: 206043 bases at least Q20		
	Insert size: 208144; sum-of-coverage		
	Insert size: 227650; 6.6% error; agarose-1p		
	Quality coverage: 5.63x in Q20 bases; sum-of-coverage		
	coverage: 5.53x in Q20 bases; agarose-1p		

	* NOTE: This is a 'working draft' sequence. It currently		
	* consists of 29 contigs. The true order of the pieces		
	* is not known and their order in this sequence record is		
	* arbitrary. Gaps between the contigs are represented as		
	* runs of N, but the exact sizes of the gaps are unknown.		
	* This record will be updated with the finished sequence		
	* as soon as it is available and the accession number will		
	* be preserved.		
	1	8088: contig of 8088 bp in length	
	*	8089: gap of 100 bp	
	*	8189: contig of 15025 bp in length	
	*	23214: gap of 100 bp	
	*	23314: contig of 3907 bp in length	
	*	27221: gap of 100 bp	
	*	27321: contig of 3006 bp in length	
	*	30327: gap of 100 bp	
	*	30427: contig of 12740 bp in length	
	*	43167: gap of 100 bp	
	*	43267: contig of 4250 bp in length	
	*	47517: gap of 100 bp	
	*	51392: contig of 3776 bp in length	
	*	51393: gap of 100 bp	

```
* 51493 60771: contig of 9279 bp in length
* 60772 60871: gap of 100 bp
* 60872 63164: contig of 2293 bp in length
* 63165 63264: gap of 100 bp
* 63265 69307: contig of 6043 bp in length
* 69308 69407: gap of 100 bp
* 69408 76647: contig of 7240 bp in length
* 76648 76747: gap of 100 bp
* 76748 98297: contig of 21550 bp in length
* 98298 98397: gap of 100 bp
* 98398 100781: contig of 2384 bp in length
* 100782 100881: gap of 100 bp
* 100882 108287: contig of 7406 bp in length
* 108288 108387: gap of 100 bp
* 108388 116410: contig of 8023 bp in length
* 116411 116510: gap of 100 bp
* 116511 119166: contig of 2656 bp in length
* 119167 119266: gap of 100 bp
* 119267 121683: contig of 2417 bp in length
* 121684 121783: gap of 100 bp
* 121784 125415: contig of 3632 bp in length
* 125416 125515: gap of 100 bp
* 125516 132751: contig of 7236 bp in length
* 132752 132851: gap of 100 bp
* 132852 137874: contig of 5023 bp in length
* 137875 137974: gap of 100 bp
* 137975 147639: contig of 9665 bp in length
* 147640 147739: gap of 100 bp
* 147740 150747: contig of 3008 bp in length
* 150748 150847: gap of 100 bp
* 150848 154411: contig of 3564 bp in length
* 154412 154511: gap of 100 bp
* 154512 180672: contig of 26161 bp in length
* 180673 180772: gap of 100 bp
* 180773 187118: contig of 6346 bp in length
* 187119 187218: gap of 100 bp
* 187219 197762: contig of 10544 bp in length
* 197763 197862: gap of 100 bp
* 197863 203431: contig of 5569 bp in length
* 203432 203531: gap of 100 bp
* 203532 206862: contig of 3331 bp in length
* 206863 206962: gap of 100 bp
* 206963 210944: contig of 3982 bp in length.

FEATURES
    source
        1. .210944
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="1"
            /clone="RP11-465B22"
            /clone_1fb="RPC1-11.2"
            1. .8088
                /note="assembly_fragment:00856
                fragment_chain:1
                clone_end:T7
                vector_side:left"
                8189. .23213
                    /note="assembly_fragment:02699
                    fragment_chain:1"
                23314. .27220
                    /note="assembly_fragment:02428
                    fragment_chain:1"
                27321. .30326
                    /note="assembly_fragment:02062
                    fragment_chain:1"
                30427. .43166
                    /note="assembly_fragment:00183
                    fragment_chain:2"
                43267. .47516
                    /note="assembly_fragment:02637
                    fragment_chain:2"
                47617. .51392
                    /note="assembly_fragment:00819
                    fragment_chain:2"

misc_feature 51493. .60771
/note="assembly_fragment:03852
fragment_chain:2"
misc_feature 60872. .63164
/note="assembly_fragment:02587
fragment_chain:2"
misc_feature 63265. .69307
/note="assembly_fragment:04648
fragment_chain:2"
misc_feature 69408. .76647
/note="assembly_fragment:00506
fragment_chain:2"
misc_feature 76748. .98297
/note="assembly_fragment:05288
fragment_chain:2"
misc_feature 98398. .100781
/note="assembly_fragment:00325
fragment_chain:3"
misc_feature 100882. .108287
/note="assembly_fragment:03939
fragment_chain:3"
misc_feature 108388. .116410
/note="assembly_fragment:01362
fragment_chain:3"
misc_feature 116511. .119166
/note="assembly_fragment:05470
fragment_chain:3"
misc_feature 119267. .121683
/note="assembly_fragment:00386
fragment_chain:4"
misc_feature 121784. .125415
/note="assembly_fragment:03427
fragment_chain:4"
misc_feature 125516. .132751
/note="assembly_fragment:00331
fragment_chain:4"
misc_feature 132852. .137874
/note="assembly_fragment:01398
fragment_chain:4"
misc_feature 137975. .147639
/note="assembly_fragment:03696
fragment_chain:5"
misc_feature 147740. .150747
/note="assembly_fragment:05495
fragment_chain:5"
misc_feature 150848. .154411
/note="assembly_fragment:00729
fragment_chain:5"
misc_feature 154512. .180672
/note="assembly_fragment:01493
fragment_chain:5"
misc_feature 180773. .187118
/note="assembly_fragment:00254
fragment_chain:6"
misc_feature 187219. .197762
/note="assembly_fragment:04216
fragment_chain:6"
misc_feature 197863. .203431
/note="assembly_fragment:00160"
fragment_chain:6"
misc_feature 203532. .206862
/note="assembly_fragment:03327"
fragment_chain:6"
misc_feature 206963. .210944
/note="assembly_fragment:04407"
fragment_chain:6"

BASE COUNT 38968 a 62852 c 66926 g 39385 t 2813 others
ORIGIN
Query Match 36.8%; Score 389.8; DB 2; Length 210944;
Best Local Similarity 76.2%; Pred.No. 3.8e-51;
Matches 609; Conservative 0; Mismatches 2; Indels 188; Gaps 3;
447 accaactgcaccttgcctgggaagacacacctgcagccggcagcaataagctcgagacga 506
|||||
```

D	b	8591	AACACTGCACCTTGGCTGGAAGCAACAACCTTGACGCCGGCCAGCAATATGCTGGACGA	8650
O	y	507	atctgttgagaaagaaggaaccccccaagcagcgagcccccaggagaaccaggggcccccgggc	566
D	b	8651	ATCTGTGAGGAAGAAGGACCCTCCACCCACCGCAGCCCCAAGAAACCAAGGGCCCCCGGGCC	8710
O	y	567	aggccaactcaactgttcagaccaccaataagccctgtagcccaagaacctcaaggaacctcaacc	626
D	b	8711	AGGCCCATTCACGTGTCCAGGCCCACTCAAGCGCTGGCCAGAACCTCACAGGAACTCTCCAC	8770
O	y	627	cggccgttggaaagtcccccgg-----	647
D	b	8771	CGGCCGTTGAGAGTCCCAGGGGGTAAGGGCCCTGTGCCAGCCAGCGGGCCCCCAAC	8830
O	y	648	-----	647
D	b	8831	CGAATAGGAAGAGGGAGGGCGGCAATTGGGGGCCCTCTCTGTGACCACCAACGACAGAC	8890
O	y	648	-----ggcglcgagltgcccgcataccttgagcctgagcctgtgtgtcgtggcgtgt	697
D	b	8891	CTTCTCTGACAGCCCTGGGGTTGGCCGCATCTCGGGCTGGGGCTGGGTCTGGGGCTGCT	8950
O	y	698	ggggcccccttgagcacaactcgt	757
D	b	8951	GGGCCCCCTGGGCACTGTCTGT	9010
O	y	758	cgattgccacaagaagccctt-----	776
D	b	9011	CGATGCCCAAGACCCCTGGTAGTGCCTATGGCCCTGGCCGCACTGCTCTGGCGGGT	9070
O	y	777	-----ggggaagagagttccggaccc	799
D	b	9071	GAGGCCCAACCAACCAATCTCTCTTTTTCTCTCCCAAGGGAGGACAGTTCTGGACCC	9130
O	y	800	catccaagaagaagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	859
D	b	9131	CATCCAAGGAGGAGCAGGCGGAGCGCCACTGCACCTGGGCAAGATCTGACC-TGGGCCCA	9189
O	y	860	ccaaggtggaagcgt	919
D	b	9190	CCMAAGGTGAGAGCTGTGGGCCCCGCCAGCGCTGGAAGCCGAGGCTGTGCTGGGCGACAGGG	9249
O	y	920	caggtgcagagccgctcgtccgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc	979
D	b	9250	CAGGTGCAGAGCGCGCTGCCGCCGCCACAGCTCTCGGGGCCAATCTGCACCGTTCTAGCTGCC	9309
O	y	980	gatgtgtccttcaggtcttgtactgatatgacatgcataccttcgtcccgaggacc	1039
D	b	9310	GATGGCTGCTCTCCGGCTCTGTCTTACGTATGCAATGATACCTCTCCCGCGCGGAGAC	9369
O	y	1040	acaatcaaaaaccttgagcag	1058
D	b	9370	AAAAAAAAACCTTGGCAG	9388
R	E	S		
L	O	C	HSA277151	5150 bp DNA linear PRI 05-JUL-2000
D	E	F	LOCUS	
I	N	T	DEFINITION	Human sapiens ox40 gene for CD134 antigen, exons 1-7.
I	N	T	VERSION	AJ277151.1 GI:8926701
I	N	T	KEYWORDS	CD134 antigen; Ox40 gene; rat Ox40 antigen homologue.
I	N	T	SOURCE	human.
I	N	T	ORGANISM	Homo sapiens
I	N	T	REFERENCE	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
I	N	T	AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
I	N	T	TITLE	Latza,U., Duxkop,H., Schnittger,S., Ringeling,J., Etelbach,F., Hummel,M., Ponatsch,C. and Stein,H. The human Ox40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen Eur. J. Immunol. 24 (3), 677-683 (1994)
I	N	T	JOURNAL	
I	N	T	MEDLINE	94170844

REFERENCE	2 (bases 1 to 5150)
AUTHORS	Pankow, R., Dirpock, H., Latza, U., Krause, H., Kunzendorf, U., Pohl, T. and Bulfone-Paus, S.
TITLE	The HTLV-1 tax protein transcriptionally modulates OX40 antigen expression
JOURNAL	J. Immunol. 165 (1), 263-270 (2000)
MEDLINE	20318724
REFERENCE	3 (bases 1 to 5150)
AUTHORS	Pankow, R.
TITLE	Direct Submission
JOURNAL	Submitted (28-MAR-2000) Pankow R., Inst. of Immunology, FU Berlin, University Hospital Benjamin Franklin, Hindenburgdamm 30, 12200 Berlin, GERMANY
COMMENT	Related sequence X75962.
FEATURES	Location/Qualifiers
SOURCE	1..5150
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
mrna	join(1267..1437,1635..1757,2228..2429,2717..2783,3284..3480,3590..3718,3797..4096)
	/gene="ox40"
	1267..4096
gene	/gene="ox40"
	1267..1292
5' UTR	/gene="ox40"
	1267..1437
exon	/gene="ox40"
	/number=1
CDS	join(1293..1437,1635..1757,2228..2429,2717..2783,3284..3480,3590..3718,3797..3867)
	/gene="ox40"
	/note="rat OX40 antigen homologue"
	/codon_start=1
	/product="CD134 antigen"
	/protein_id="CAB96543.1"
	/db_xref="GI:8926702"
	/translation="MCVGARRLRGPGCAALLLGISTVNGLHCVGDTYPSNDRCCHECRGNGNVSCHSRSONTVCRPCGPRFNDVSSKRPCRCYMCNLRBSSEKQCTARQDVIKCRKAGTQPLDSTRPGVDCAKCPFGHSPEDNQCCKFWTCLGKHTLDPASVSSDIICEDRDPPATQPOETGPPARPIVQPTETAMPRTSGSPSTRPEVPGGKVAALALGCLIVGLGLCPALILALYLLRRDORLPPDAHKRPGGSPFRPIEODADAHSTLAMI"
intron	1438..1634
	/gene="ox40"
	/number=1
exon	1635..1757
	/gene="ox40"
	/number=2
intron	1758..2327
	/gene="ox40"
	/number=2
exon	2328..2429
	/gene="ox40"
	/number=3
intron	2430..2716
	/gene="ox40"
	/number=3
exon	2717..2783
	/gene="ox40"
	/number=4
intron	2784..3283
	/gene="ox40"
	/number=4
exon	3284..3480
	/gene="ox40"
	/number=5
intron	3481..3589
	/gene="ox40"
	/number=5
exon	3590..3718
	/gene="ox40"
	/number=6
intron	3719..3796

Db	301	ACTGCTGCAGATGTATAGACCGGACCCAACTGCGGACGACAGCGGCTTACAAAGCTTGG	360
OY	381	gttactgtgtccccctgtccctccagggaacttctccaggcgacaacaaagcgcctgcaag	440
Db	361	GTTCACGTGTGTTCCCTCCCTCCCTCCGCGCACTTTTCTCCAGGCAAAACACAGGCTCGAAG	420
OY	441	ccccgtgagccaactgtcaccttggcgtgggaagacacaccccttgacgcgcgcgaataagctcg	500
Db	421	CCCTGGACCAATTTTACCTTATCTGGAAACAGACCGCGACCCAGCCAGCACTGACACTTG	480
OY	501	gacgcacatctgtgagacagagacccccgcacgcagcccgagaccgaagaccgaagccccc	560
Db	481	GACCGCACTGTGTGAGACAGAGAGCCTCTCTGGCCACACTGCTCTTGGGAGACCCAGCGCCT	540
OY	561	ccggccagagcccatcactgtgtccagcccacatgaaagcctgtgcccagaactcacagggaacc	620
Db	541	ACATTCAAGGCCAACACAGCTGTCATTCACACAGTCTGCGCCAGAGATTGTGAGTTGCC	600
OY	621	tccaccgcgcgttggaggtcccccgggggcgtgtcgtgtgcgcacatccttggccttggc	680
Db	601	TCTCCACCACACTTGTGTGACTCTCGAAGGGCCCTGCATTGTCTTCTCAAGGCTTGGGC	660
OY	681	ctgtgtctgtggggtgcgtcgtgggcccccttggccatcctgtgttggcctgtacatcgtcctcggag	740
Db	661	-----CTGGGCTCTGTGGGCTCCCTTACCTGTCTGCTGGGCTTTGATCACTGCTCCGGAAG	714
OY	741	gaccagaagctgtcccctccgatgtgccaaagcccccttggggaggaagctttccggaacccc	800
Db	715	GCTTGGAGATTG---CCTAACCTCTCCAAACCTGTGTGGGGGAAACAGCTTCAGAGACCCG	771
OY	801	atccaaaggaagcagcgccagcgcacatcaaccccttggccaagatctgtaccttgggtccac	860
Db	772	ATCCAGGAGGAAACACAGACAGCACTTACTCTGTGGCAAGATCTGAGCATTTAGTACAG	831
OY	861	caagtgtagacgtgtggccccg	881
Db	832	GAGTGGATTATATGGGGGCAC	852

[illegible]

Db	181	CATCCGCTGAGACTGGCTTTACAATAAGAACTGTCAATTATGATTAAGTACCTCCAAAGCACTGT	240
Qy	267	acgttggtgtaacctcaagaagctgggagtgagaggaagcagctgtgacagcgacacacagagac	326
Db	241	ACACAGTGCAMACATCGAAGTGAAGTGAAGTAAGTAACGAAGCAAGATTGCACACTACTCAAGAT	3000
Qy	327	acagctctgcgcgtccgcggggcgagcaccaccgcttga-----cagctacaagcttga	3800
Db	301	ACTGTCCTCAAGATGATGAGCCAGGACCCCAACCTCTGGCAGGACACAGCGGCTCTCAAGCTTGGA	3600
Qy	381	gttagctgtgccccctgcccccccaaggagacactctcccaaggagacaaacagagctgtgaag	4400
Db	361	GTTCAGCTGTGTTCCCTGCCCCCTCTCGGCCACTTCTCTCAAGGACAAACACAGGCTTGAAAG	4200
Qy	441	cccttgaccacaactgcacacttgccttgggaaagacacacccttgcagccggcgacaaatagctcg	5000
Db	421	CCCTGGACCAATTGTACTTATCTGGAAGAAGACAGACCCGCCACCCAGCCAGCAAGTGAAGCTTG	4800
Qy	501	gaagcaactcttgaagagacagagagaccccccaagcagaagcccccaagagagacccagagcccc	5600
Db	481	GACGCAAGTCTGTGAGGAGACGAAGGCTCTCTGGCCCACTGTGCTCTGGGAGACCCAGGCGCTT	5400
Qy	561	ccggcgcaaggccatcaactgctccagcccaactgaagccctgggcccacgaacactcaagagagccc	6200
Db	541	ACATTCCAGGCCAACCCAGCTGTCCATTCCACACCAAGTCTGGCCCAAGGACTTTCGAGTTGCC	6000
Qy	621	tccacccggccccgttgaaggtcccccgggggcccgttgcgttgcgcacactcttgggccccttggc	6800
Db	601	TCTTACACCCACACTTGGTGGAGACCACGAGTCTGTGACAAAAACTCACACATGCCCCACCGTGC	6600
Qy	681	ctgtgtgctggggctgtgtggccccctggccatctctgtgtggccc	723
Db	661	CCAGCACTTGAAGCCGAGAGGGCGCGCCGTCAGTCTTCTCTTCC	703

LOCUS	114936	1317 bp	DNA	linear	PAT 02-APR-1996
DEFINITION	Sequence 10 from patent US 5457035.				
ACCESSION	114936				
VERSION	114936.1	GI:1249844			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 1317)				
TITLE	Baum,P.R., Fanslow,M.C. III, Gayle,R.B. and Goodwin,R.G.				
JOURNAL	Cytokine which is a ligand for OX40				
FEATURES	Patent: US 5457035-A 10-10-OC-1995; Location/Qualifiers 1..1317 /organism="unknown"				
BASE COUNT	322 a 417 c 337 g 241 t				
ORIGIN					
Query Match	27.1%;	Score 286.6;	DB 6;	Length 1317;	
Best Local Similarity	66.6%;	Pred. No. 8.5e-35;			
Matches 428;	Conservative 0;	Mismatches 209;	Indels 6;	Gaps 1;	
Qy 87	accgtagacggggtccactcgtgtgcggagacatcccccagaacgacacgcggtgcgcac	146			
Db 61	acagcagaagcggcctcaactcgtctttaacatraccttaccacagtggtcacagaagtcgtcgt	120			
Qy 147	gagtcgaagccagagaacggaatggtlgaacgcgttcagacgcgtccccaagaacacggtgtgc	206			
Db 121	gagtcgacacccagaccatcgtatggtgaacccctcgtgatcatcaccagggatcctatgt	180			
Qy 207	cgctcgtgtagggccggggtcttacaacgaacgtggttcacgtccaaagccgtlgaacgcctgc	266			
Db 181	catccgctgtgagactggcctcttaccatgatgaagctgtcaattatgatgactcgaagcagtg	240			

OY	267	acgtggtctaaacctcaagaaatgaggagtgagcggaaagcagctgctgacggccacacagagac	326
Db	241	ACACAGTCAACCAATCGAAGTGAAGTAAGTCAACGACGAATTTGCACACTTACAGGAT	300
OY	327	acagctctgcgcctgcgcggcgcgagccaccagccctctgga-----cagctacaagccttga	380
Db	301	ACTGCTCGAGATGATGAGACACAGGCCACCCCAACTCTGGCAGGACAGGGCGCTACAAAGCTTGA	360
OY	381	gttgactgtgcctccctctgcccctccacaggcaactctctcccaagsgaataacacagcctcgcaag	440
Db	361	GTTGACTGTGTTCCCTGCGCCTCTCCTGGCCACTTTTCTCAAGGACAAACACAGGCTGTGCAAG	420
OY	441	cccttgagacaaactgcacactctgctctgtagaagcacaacacctgcagccggcagcaatagctcg	500
Db	421	CCCTGGACCATTGTGACTTATCTGTGGAAGCAGACCCGCCACACCCAGTATACAGCTTGG	480
OY	501	gaacgaacatctgtgagagacagagaaacccccagccacgcagcccccaaggagaacccagggcccc	560
Db	481	GACGGAGTCTGTGAGGACAGAAAGCTCTCTGGGCCACACTGCTCTGTGGAGAACCCACGAGCCCT	540
OY	561	ccggccagagccacatacactgtccagccacactgaagccttgcggccagagactcaagagaaaccc	620
Db	541	ACATTCAAGGCCAACCACTCTGTCATTCACACACAGTCTTGCCACGAGACTTCTGAGTTGGCC	600
OY	621	tccaccccgagcccgctggaaggtgccccggggggcgctgctgctgcgcgcacatcctgggaccttgagc	680
Db	601	TCTACACCCACACTTGTGGTGGAGCCCGAGATCTGTGTGCAAAATCTCACACATATGCCACCGTGC	660
OY	681	ctagtgtcgtggggctgctgtagcccccctgtgcacatccctgcctgcggccc	723
Db	661	CCAGCACTCTGAAGCCGAGAGGGCGCGCGCTGACGTCTTCTCTCTTTC	703

[illegible]

OY	327	acagctctgcgcctgtgcggggcgggacacccgaccccttgg-----cagctaaacgcttga	380
Db	301	ACTGCTGCAGATGATGAGACACAGCACCCACACTCCGGCAGACAGGGGCTTACAACTTGA	360
OY	381	gttgacatgtgcccccctgcacctccacaggacattctctccaaagcgacacaccagccttgaag	440
Db	361	GTTCAGTGTGTTCCCTGGCTCTCTGGCCACATTTCATCAGGCAACAAACAGGCCATGACAAG	420
OY	441	cccttgaccacacatgtcaccttgtcttggaaagcacacaccttgcagccggccagacatagtctcg	500
Db	421	CCCTTGACCACATTGTACTTATCTGTGAAAGCAGACCCGGCACCCAGCAGTGATGACGCTTG	480
OY	501	gaacgcaatctgttgaagaacagggaacccccacagcccaagcagccccaaagagaaccagggcccc	560
Db	481	GACGCAAGTCTGTGAAGACAGAAAGCTCTCTGGCCACACTGTCTTGGAGAACCCAGGCGCTT	540
OY	561	ccggccagggccacatcattgtccagcccacttgaagccttggcccaagaccttcacagggacc	620
Db	541	ACATTCAGAGCCCAACCACTGTCCAAATCCACACACAGTGTGAGCCACGAGCATTTCTGATTTGCC	600
OY	621	ttcacaccggccgctgtgag	638
Db	601	TTCTACACCCACCTTGTGTG	618

[illegible]

Db	361	GTGACGTGTGTCCTCCCTCCCTGGCCACTTTTCTCCAGGCAACAAACAGGCGCTCGAG	420
Oy	441	cccttgaccactgacaccttggcttgggaagacacccctgcagccggcagaatagctg	500
Db	421	CCCTGGACCAATTGTACTTATTGTGAAACAGACCCGCCACCCAGCCACTGACACTTG	480
Oy	501	gaaccaatctgttagagacagagacccccccagcccaagcagcccggaagagaccagagcccc	560
Db	481	GACCGACTGTGTGAGGACAGAAAGCCTCTTGCCACACTGCTCTTGGGAGACCCAGCGCCT	540
Oy	561	ccggccagcccatcactcgttccagcccaatgaagcttggcccaagaacctcacagggacc	620
Db	541	ACATTTCAGGCCCAACCACTGTGTCATCCACACAGCTGTGGCCAGGACTTGTGATTGCC	600
Oy	621	tcaacccggccgctggag	638
Db	601	TTCTACCCCACTTGGTG	618

RESULT	15			
LOCUS	AX251336/c			
DEFINITION	Sequence 304 from Patent WO0168912.	6080 bp	DNA	
ACCESSION	AX251336			linear
VERSION	AX251336.1			PAT 05-OCT-2001
KEYWORDS	GI:15984759			
SOURCE	.			
ORGANISM	synthetic construct. synthetic construct.			

	Query Match	Similarity	11.8%	Score	124.4	DB 6	Length	6080
	Best Local	Similarity	74.8%	Pred.	No.	3.7e-10		
	Matches	169	Conservative	0	Mismatches	55	Indels	1
								Gaps
								1
QY	832	cccttgcgaagaatctgacacttggccccaacgaagtgcagctgggcccgcgcagctgga	891					
Db	6080	CCCTTACCAAAATCTTAACGCTAAACCCCAAAAATTAACGCTAAACCCCGCAAACTTAA	6022					
QY	892	gcccggaagggtctgtgtggcgagcagggcaggtgtgaagcgcgctgcgccgcgcagctcct	951					
Db	6021	ACCCGAAAAATCTACTTAAACGAACAAACAAATATCAACACCGCTACCCCGCACGCTCT	5962					
QY	952	gggcgaactctgcacgcgttctagtgtagcgcgatgctgcgcctcgcgcctctctgctactg	1011					
Db	5961	AAACCAACTCTACACCGCTCTTAATATACGATTAACCTACGACGACGCTCTACTTACGTATA	5902					
QY	1012	ccatgcatactcctctgcgccgcgggagccacgaataaaaccttggca	1057					
Db	5901	CCATGCATATACGCTCTACACCGCGGAAACCAACATATAAAACCTTTAACA	5856					

Search completed: June 18, 2002, 18:44:09
Job time: 14967 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 14:34:42 ; Search time 1939.35 Seconds
(without alignments)
7363.178 Million cell updates/sec

Title: US-09-852-845-1
Perfect score: 1058
Sequence: 1 cagcagagcagcagatgtgc.....cacataaaacctgtgcag 1058

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	615.6	58.2	844	9	AT1738634
C 2	564	53.3	743	10	BI833441
C 3	540	51.0	569	10	BI833441
C 4	526.4	49.8	544	10	BI833441
C 5	498.4	47.1	893	10	BI833441
C 6	495	46.8	512	10	BI833441
C 7	417.6	39.5	471	9	AM293499
C 8	352.2	33.3	668	9	AT1991307
C 9	331.6	31.3	398	9	AA970291
C 10	305.4	28.9	353	9	AM290885
C 11	298.2	28.2	347	9	AA452801
C 12	289.4	27.4	393	9	AA306055
C 13	282	26.7	630	9	AA501118
C 14	214.8	20.3	609	9	AT323590
C 15	206.4	19.5	247	9	AT1914208
C 16	178.6	16.9	198	9	AM591834
C 17	145.2	13.7	172	10	BI824093

C 18	139	13.1	560	9	AM743856
C 19	135.4	12.8	511	10	BM285756
C 20	130	12.3	423	9	AA110765
C 21	130	12.3	459	9	AT323199
C 22	92	8.7	92	10	BI821828
C 23	85.4	8.1	414	9	BE095512
C 24	81.4	7.7	459	9	AM744325
C 25	74.6	7.1	925	12	CNS0091P
C 26	74.6	7.1	1389	10	BM624255
C 27	70.4	6.7	925	12	CNS0091P
C 28	68.6	6.5	935	12	CNS006X
C 29	65.2	6.2	888	12	AG030591
C 30	64.8	6.1	776	12	CNS010RY
C 31	64.8	6.1	932	12	CNS00720
C 32	64.2	6.1	935	12	CNS006X
C 33	64.2	6.1	1203	12	CNS015V4
C 34	63.4	6.0	885	12	AG159162
C 35	63.2	6.0	313	9	BI164410
C 36	63	6.0	1137	10	BM809979
C 37	61.6	5.8	1389	10	BM624255
C 38	61	5.8	911	12	AG043617
C 39	60.8	5.7	691	12	AG171171
C 40	60.8	5.7	724	12	AG171201
C 41	60.8	5.7	978	12	AG030617
C 42	60.6	5.7	613	12	AG043036
C 43	60.6	5.7	817	12	AG140822
C 44	60.6	5.7	1100	12	AG161988
C 45	60	5.7	1101	12	CNS01523

ALIGNMENTS

RESULT 1
AT1738634/c
LOCUS
DEFINITION
w111d02.x1 NCI-CGAP Co16 Homo sapiens CDNA clone IMAGE:238923 3'
similar to SW:OX40.HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains
MER22.t3 MSRI repetitive element ;, mRNA sequence.

ACCESSION
AT1738634
VERSION
AT1738634.1 GI:5100615

KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
1 (bases 1 to 844)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

AUTHORS
TITLE
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index

JOURNAL
COMMENT
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/dbtrp/image/image.html

Insert Length: 1075 Std Error: 0.00
Seq primer: -40up from Gibco
High quality sequence stop: 452.

Location/Qualifiers
1..844

FEATURES

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:238923"
/clone_lib="NCI-CGAP Co16"
/tissue_type="Colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_C010 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1057416-1061255, and 114584-114531).

Subtraction by Bento Soares and M. Fatima Bonaldo. " BASE COUNT 139 a 245 c 302 g 154 t 4 others

Query Match 58.2%; Score 615.6; DB 9; Length 844; Best Local Similarity 93.6%; Pred. No. 3.4e-98;

Matches 661; Conservative 0; Mismatches 43; Indels 2; Gaps 2;

353 ccagcccccgtgagcttacaagcctgtagtctgctccctcctcctcagggagcact 412
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 704 CCCACCCCTGCGCAGTTACATAGCTGGAG-TGCTGTGTCACCTGCCCCCTTACAGTGCATTTC 646
413 ctcccaaggcgaacaacagagcctgcaagcctggaaccaactgacacttgctggagaaga 472
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 645 TCCCGAGTGAACAGAGCCCTTCCAGACATGAGCACTGGACCTTGNTGGAGCGCA 586
473 caacctgcaagccggcgaacaataagctggaagcaatctgtgagagcagagagcccccagc 532
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 585 CACCATGCAAGCGCGGACGAATAGCTCGAGCCCAATCTGTGAGAGACAGGACCCCCACAC 526
533 cagcagcccaaggagaagcccaaggcccgcccgccagcccaactgctcagcccaactga 592
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 525 CACGCAAGCCCAAGAGACCCAGAGGCCGCCCGGCAAGCCCATCTGTCCAGCCCAANTBA 466
593 agcctggcccaagaacctcacaaggagacccctcaccgcccgttggaggctcccgaggccg 652
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 465 ACGNTGGCCCAACACTCACAGGAGACCTCCACCCCGCCGTTGGAAGTCCCGGGGGCCG 406
653 tggaggttgcgcgaatcctgagcctgagcctgtgtgctggagcctgagcctcctggagcct 712
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 405 TCGGCTTGCCTGCATCTCTGGGCTTGCGCTGTGCTGGGCTGTGCTGGCCCTTGCCAT 346
713 cctgtcgtgcccctgtacactcctcgcgaaggagacagagctgcgcccgcgaatgcccacaagc 772
345 CCTGTGCGCCCTGTACTCTCTCGGAGGAGACCAAGAGCTGCCCGCGATGCCACAGCC 286
773 cccctggggaggagcagttcttcggaagccccaacccaagaagagagcagcgcccaactcaac 832
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 285 CANTGGGGAGGACAGTTTCCGAGACCCCATTCACAGAGGAGGAGGCCGACGACATCCAC 226
833 ccttggcccaagatctgacacttggccccaagagtgagacgttggcccgccagagctggag 892
225 CCTGGCCAAAGATTGTGAC-TGGGCCCAACCAAGGTGAGCTTGCGCCCGCCAGGCTGGAG 167
893 ccgagagaggtctcgtcgtgagcgaagagcaggtgcagcgccctgcccgcgaacgctcctg 952
166 CCGGAGGGTCTGCTGGGAGAGAGGAGGTGACAGCGCGCTGCCCGCCAGCGCTCG 107
953 ggcacaactctgacagcttctagtgccgaatggtcgtcctcggcctctcgtcttaagctatc 1012
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 106 GCCCAACTCTGACAGCTTCTAGTGGCCGATGCTGCTCGGCTCTCTTACGATATGC 47
1013 catgtacactctctgcccgcggagccacaataaacttggcag 1058
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 46 CATGTACTCTCTCTGCGCCGCGGAGACCAATMAAACTTGGCAG 1

RESULT 2
BI833441 743 bp mRNA 1linear EST 04-OCT-2001
LOCUS 60308095F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5227199 5',
DEFINITION mRNA sequence.
ACCESSION BI833441
VERSION 81833441.1 GI:15944991
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 743)
AUTHORS NIH-MGC http://mgi.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLM11571 row: m column: 24
High quality sequence stop: 659.

FEATURES
source
1. 743
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5227199"
/clone_1lb="NIH_MGC_120"
/lab_host="DH10B"
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb. Insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."

BASE COUNT 135 a 275 c 235 g 98 t

Query Match 53.3%; Score 564; DB 10; Length 743; Best Local Similarity 95.2%; Pred. No. 3.5e-89; Matches 668; Conservative 0; Mismatches 25; Indels 9; Gaps 8;

353 ccagcccccgtgagcttacaagcctgtagtctgctccctcctcctcagggagcact 412
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1 CCAGCCCTGAGACAGCTTAAAGCTGTGACTGTGCTGCCCTGCCACAGG-ACCT 59
413 ctcccaaggcgaacaacagagcctgcaagcctggaaccaactgacacttgctggagaaga 472
|| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 60 CTCGCCAGGCGACACACAGGCTCGAAGCCCTGACCACTGACCTTGCTGGAGAGCA 119
473 caacctgcaagccggcgaacaataagctcgaagcgaactctgtgaggaagagagcccccagc 532
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 120 CACCTGCAAGCGCGCAGCAATAGCTCGAGCAATCTGTGAGAGACAGGAGCCCCACAG 179
533 cagcagcccaaggagaagcccgcccgcccgccagagcccaactgctcagagcccaactga 592
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 180 CACGCAAGCCCAAGAAACCA-GGCCCCCGGCAAGCCCATCTACGTCCAGGCCACTGA 238
593 agcctggcccaagaacctcacaaggagacccctcaccgcccgttggagggtcccgaggccg 652
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 239 AGCTTGCCCAAGACTTCAAGGAGACCTTCACCCGCGCTGAGAGTCCCGGGGGCCG 298
653 tggaggttgcgcgaatcctgagcctgagcctgtgtgctggagcctgagcctcctggagcct 712
299 TGGGTTGCGCGCATCTGAGGCTTGCGCTGTGCTGGGCTGTGCTGGCCCTTGCCAT 358
713 cctgtcgtgcccctgtacactcctcgcgaaggagacagagctgcgcccgcgaatgcccacaagc 772
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 359 CTTGTGCGCCCTGTACTCTCTCGGAGGAGACCAAGAGCTG-CCCGGATGCCCAAGGCC 417
773 cccctggggaggagcagttcttcggaagccccaacccaagaagagcagcgcccaactcaac 832
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 418 CCTGGGGGAGGAGTTCCGACCCCATCCAGAGAGAGAGGCGGACGCCACTCCAA 477
Qy 833 cctggcaagaatctgaccttgcccccagaagtggagctggcgcccgcaagctgag 892
Db 478 CCTGGCCCAAGATCTGACC-TGGGCCCAACCAAGGTGAGCTGGGCCCGCCGAGGTGAG 536
Qy 893 cccggaaggtctgtggtgagcagagggcagag--tgcaagcgccgtccgcacgcctcc 950
Db 537 CCCGAGGAGGCTGGCTGGGGCGAGAGGAGGTTGACAGGCTGCGTG-CCCGGACAGCTCC 595
Qy 951 tggcgcaactctgacgcgttcta-gtgcgagatggctgctcgcggtctctgttaagta 1009
Db 596 TGGGCAACACTGCGACCGGTCTAGGCTGTCGATGGCTGGCTCTGTGTACGTA 655
Qy 1010 tgcatactctgcccgcgagagcacaataaanaac 1050
Db 656 TGCATGTCATTAATCTCTGGCCCGGAGGACAGCAATTAAC 697

RESULT 3
Bg236062/c
LOCUS
DEFINITION Bg236062 569 bp mRNA linear EST 12-FEB-2001
naif22a07.x1 Soares_NPBMC Homo sapiens cDNA clone IMAGE:4141716 3'
similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains
MER22.t1 TARI repetitive element ; mRNA sequence.
ACCESSION Bg236062
VERSION Bg236062.1 GI:12749909
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheraia; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 569)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D. and M. Fatima
Bonaldo, Ph.D.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
info@image.jnl.gov
Seq primer: -400P from Glibco
High quality sequence stop: 478.
location/Qualifiers
FEATURES
source
1..569
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4141716"
/clone_id="Soares_NPBMC"
/tissue_type="Lymphocyte"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pT7TD-pac; site:1: NotI;
site:2: EcoRI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5'
TGTACCAATCTGAAGTGGAGCGCGCGGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
is normalized; constructed in the laboratory of M. Bento
Soares (University of Iowa)."

BASE COUNT 78 a 179 c 223 g 89 t
ORIGIN

Query Match 51.0%; Score 540; DB 10; Length 569;
Best Local Similarity 99.8%; Pred. NO. 5.2e-85;
Matches 551; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 507 atcttgagagacagggaccccccaagccacgcagcccccaagagaccccaagggcccccggcc 566
Db 509 ATCTTGGAGACAGGAGACCCCCCACCACAGCCAGCCAGAGACCCAGAGGCCCCCCGGGCC 510
Qy 567 aggcccaatcactgtlcccaagccactgaagccttggtcccaagaactcaagaagacccctcaac 626
Db 509 AGGCCATACACTGTCCACCCACCTGAACCTTGCGCCACAAACCTCAAGAGGACCTCCACAC 450
Qy 627 cggcccgatgaggttcccccgggggcccgtgaggttgcgcacatccttggtggtggtg 686
Db 449 CGGCCCTGTGAGGTCCCGGGGGCGCTCGGTTGCCGCAATCTTGCGCTGGGCTCGGTG 390
Qy 687 ctggagctgctggggccctctgcaatctgtctggtggtggtggtggtggtggtggtggtggtg 746
Db 389 CTGGGGCTGCTGGGCCCTTGCGCAATCTGTGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTG 330
Qy 747 agctgtccccccgatlcccaagaagcccccttggtggtggtggtggtggtggtggtggtggtg 806
Db 329 AGGCTGCCCGCCGATGCCACAGCCCGCTGGGGAGGCAATTCGGAGCCCGCATCCAA 270
Qy 807 gagagagagagcagagcccaactccaccccttggtggtggtggtggtggtggtggtggtggtg 866
Db 269 GAGGAGCAGGCGCAGCCACCTCCACCTGGCCAAAGATCTGACC-TGGGCCCAACCAAGGT 211
Qy 867 ggaagctggcccccgccagagctgagagcagaggttctgtggtggtggtggtggtggtggtggtg 926
Db 210 GGACGCTGGCCCCCGCCAGGCTGGAGGCCGAGAGGCTGTGCTGGGAGCAGGCAAGGTGC 151
Qy 927 aggcgcctgtcccgccagcagcgtctgtggtggtggtggtggtggtggtggtggtggtggtg 986
Db 150 AGGCGCGCTGCCCGCCAGCGCTCTGGGCAACCTGTGACCGCTGTAGGTGGCGATGGCT 91
Qy 987 gcttcggtctctgtcttactgcatgtatgcatgcatgcatgcatgcatgcatgcatgcatgcatg 1046
Db 90 GCCTCGGCTCTGTGCTTACGATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCA 31
Qy 1047 aaacttgagcag 1058
Db 30 AAACCTTGGCAG 19

RESULT 4
BF063899/c
LOCUS
DEFINITION BF063899 544 bp mRNA linear EST 16-OCT-2000
7hp0a10.x1 NCI-CGAP_CO16 Homo sapiens cDNA clone IMAGE:3323226 3'
similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains
MER22.t1 PTR5 repetitive element ; mRNA sequence.
ACCESSION BF063899
VERSION BF063899.1 GI:10822809
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheraia; Primates; Catarrhini; Homindae; Homo.
REFERENCE 1 (bases 1 to 544)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NATIONAL Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN, send email to:
info@image.jnl.gov
Seq primer: -400P from Glibco
High quality sequence stop: 423.
location/Qualifiers
FEATURES

Oy	940	cggcagctcctgaggccacactcgacgcgttcagtgtgcgatagctctccggctctc	999
Dd	144	CCCCAGTTCCTTGGGCCCAATTTTGCCTCGCTTTTAGTGTCCAGATGCTCCTCGGCTTTT	85
Oy	1000	tgcctacctatcgcatatcacctctgcccgcgcgcgcacacaataaaccttgccag	1058
Dd	84	TGCTTACTATGCGCATGATACCTCTCTCCGCCGCGGACCACCAATATAAACCTTGCGACG	26
RESULT	9		
AA970291/c		398 bp	mRNA linear EST 20-MAY-1998
LOCUS		op09ph05.s1 NCI CGAP Kid6 Homo sapiens CDNA clone IMAGE:1575225 3'	
DEFINITION		similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; , mRNA sequence.	
ACCESSION		AA970291	
VERSION		AA970291.1	GI:3145804
KEYWORDS		EST.	
SOURCE		human.	
ORGANISM		Homo sapiens	
REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS		1 (bases 1 to 398)	
TITLE		NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.	
JOURNAL		National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index	
COMMENT		Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgapbs@email.nih.gov Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Stratagene, Inc. CDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: www-bio.llnl.gov/dbfp/image/image.html Seq primer: -40ml3 fwd. RT from Amersham High quality sequence stop: 180. Location/Qualifiers 1..398 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:1575225" /clone_lib="NCI_CGAP_Kid6" /sex="mixed" /tissue_type="kidney tumor" /lab_host="SOLR (kanamycin resistant)" /note="Organ: kidney; Vector: Bluescript SK-; Site:1; EcoRI: Site_2; XhoI: Cloned undirectionally. Primer: Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5' GAATTCGGACGAG 3' 3' adaptor sequence: 5' CTCCAGTCTTTTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."	
FEATURES			
Source			
Query Match		31.3%; Score 331.6; DB 9; Length 398;	
Best Local Similarity		94.0%; Pred. No. 1.3e+48;	
Matches 378; Conservative		0; Mismatches 19; Indels 5; Gaps 3;	
Oy	648	gaccctgsgattgccgcacatcctctgagcctgagcctgctgagcctctgagccctctg	707
Dd	398	GGGCCATTGGTTCGCCCATCTCTGGGCTTGGGCTGTGAGCTGAGCTAGTGGCCCTTG	339
Oy	708	gccatctctgtagcccttacctgctccggagggagacagagctccccccgatgcc-a	766
Dd	338	GCAATCTGCTGGGCGCTTACCTGCTCGGAGGAGCACAGAGCTGCCCCCGATGCCAA	279
Oy	767	caagcccccctggggaggaagcagttccggaaccccatccaagaagagcagccgaccca	826
Dd	278	CAAAGACCCCCTGGGGAGGACAGTTTCCGAGACCCCAATCCAAGAGGAGCAGGCCGAGCCAA	219

QY	827	ctcaacccctggccaagatctgaacttgggccaccacaagtgtygaagctctggcccccgaag	886
Db	218	CTCCACCCCTGGCCAGAGACTCTGCAC-TGGGGGCGACCAAGAGTGGACGCTGGGCCCGCCGACG	160
QY	887	ctgagagcccggaagggtctgctctggcgagcagaagcgatgacagcgccgctctgcccgacag	946
Db	159	CTGGAGCCCGGAGGCTCTGCTGTGGCGACACAGGAGGTGCGAGCCGCTTGCACGCCACAG	100
QY	947	ctctctggcgcaactctgacccgtctcaagtgtcgcatgctcctctcctcctcctctgcttac	1006
Db	99	CTCCGTGGGCGCAACTCTGCACCGTCTTAGTCCGAGTGC---ACGTCCGGCTCTGCTGCTTAC	43
QY	1007	gtatgccatgcatactctctctgcccgcgagaccacaataaa	1048
Db	42	GTATGCCATGCATACCTCTGCGCCGCGGAGACACAAATMAAA	1
RESULT	10		
LOCUS	AM290885/c	353 bp	linear
DEFINITION	U1-H-B12-aggd-b-03-0-U1.s1 NCI-CGAP-Sub4 Homo sapiens cDNA clone		EST 16-JAN-2000
ACCESSION	AM290885	IMAGE:2723669 3', mRNA sequence.	
VERSION	AM290885.1	GI:6697521	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Cetiata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgaabs-remail.nih.gov		
	The sequence contained an oligo-dT track that was present in the		
	oligonucleotide that was used to prime the synthesis of first		
	strand cDNA and therefore this may represent a bonafide poly A		
	tail. cDNA library Preparation: M.B. Soares Lab Clone distribution:		
	NCI-CGAP clone distribution information can be found through the		
	I.M.A.G.E. Consortium/LLNL at:		
	www-bio.llnl.gov/bnbp/image/image.html		
	Seq primer: M13 Forward		
FEATURES	Location/Qualifiers		
source	1..353		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2723669"		
	/clone_lib="NCI-CGAP-Sub4"		
	/lab_host="DH10B (Life Technologies)"		
	/note="Vector: pT7T3D-Pac (Pharmacia) with a modified		
	polylinker; Site.1: Not I; Site.2: Eco RI; The		
	NCI-CGAP Sub4 library is a subtracted library derived from		
	the NCI-CGAP Sub2 library which is a subtracted library		
	derived from the NCI-CGAP Sub1 library, which is a		
	subtracted library derived from BI. BI constitutes a		
	mixture of 21 normalized or subtracted NCI-CGAP		
	libraries: NCI-CGAP_C04, NCI-CGAP_P122, NCI-CGAP_P128,		
	NCI-CGAP_C010, NCI-CGAP_C016, NCI-CGAP_K1d5,		
	NCI-CGAP_K1d12, NCI-CGAP_K1d3, NCI-CGAP_K1d11,		
	NCI-CGAP_Lym2, NCI-CGAP_B12, NCI-CGAP_C08, NCI-CGAP_CLL1,		
	NCI-CGAP_Le12, NCI-CGAP_Brn23, NCI-CGAP_Lu5,		
	NCI-CGAP_Lu24, NCI-CGAP_Lu19, NCI-CGAP_GC4, NCI-CGAP_GC6,		
	NCI-CGAP_Brn25. These 21 libraries were pooled and a		
	single-stranded DNA preparation of the resulting mixture		
	was used as a tracer in a subtractive hybridization with		
	a driver whose composition is detailed below:		
	NCI-CGAP_K1d3 pool 1 : LHAM 3334-3337, 3682-3683,		
	3798-3803 (IMAGE cloneIDs 1322376-1323911,		
	1456008-1456775, 1500552-1502855) NCI-CGAP_K1d5 pool 1 :		

O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A., Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geophagen, N.S., Glodak, A., Gnehm, C.L., Hanna, M.C., Hedblom, E., Hinkle, P.S., Jr., Kelley, J.M., Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M., Moreno-Palauques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M., Phillips, C.A., Ryder, S.E., Scott, J.L., Saudak, D.M., Shirley, R., Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y., Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J., Dunke, D., Feng, D.-F., Ferrite, A., Fischer, C., Hastings, G.A., He, N.W., Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H., Raymond, L., Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillion, P.J., Fannon, M.R., Rosen, C.A., Haseltine, W.A., Fields, C., Fraser, C.M. and Venter, J.C.

TITLE Initial assessment of human gene diversity and expression patterns based upon 83 million nucleotides of cDNA sequence

JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)

MEDLINE 96026280

COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerlav@tigr.org
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (<http://www.tigr.org/tdb/hgl/hgl.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
1. .393
/organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_id="jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 73 a 151 c 124 g 45 t

ORIGIN

Query Match 27.4%; Score 289.4; DB 9; Length 393;
Best Local Similarity 99.7%; Pred. No. 3e-41;
Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 281 cagaagtggagtgagcggaaagcgtgtgtcagggcacacagacagcagctgcgctg 340
|||||
Db 103 CAGAAGTGGAGTAGCGGAGAGAGCTGTGCACGGCCACACAGACAGCTGCCGCTG 162
|||||

QY 341 ccggggcgagccagcccgagcagctagaagcgtgtgtgtgtgtgtgtgtgtgtgtgt 400
|||||

Db 163 CCGGGGGGGACCCAGCCCTGGACAGCTGACCTGAGTGTGCTGCCCTGTGCC 222
|||||

QY 401 tccagggcactcttccagagcgacaacagcgctgcagccctgtgacaactgtcactt 460
|||||

Db 223 TCCAGGGGACCTTCTCCAGGCGACACACAGGCTGTGCAAGCTGTGACCACTGCACTT 282
|||||

QY 461 ggtctgggaagcacacccctgcagcgccgagcaaatagctcgagcgaactctgtgaagacag 520
|||||

Db 283 GGCTGGGAGACACACCTGCGAGCGGGCAGCAATAGCTCGAGCGCAATCTGTGAGAGACAG 342
|||||

QY 521 ggaaccccccaacagcagcccccaagagagaccagggcccccccgagcagcc 571
|||||

Db 343 GGACCCCGCCACGACGACGCCCGCAGAGACCCAGGCGCCCGCGGACGAGCC 393
|||||

RESULT 13

AA501118 630 bp mRNA linear EST 01-JUL-1997
LOCUS AA501118
DEFINITION v197h05.t1 Soares_mammary_gland_NbMNG Mus musculus cDNA clone
IMAGE:851769 5' similar to gb:z21674 M.musculus OX40 (MOUSE);, mRNA

sequence.
AA501118
VERSION AA501118.1 GI:2236085
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE
AUTHORS Maira, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE The Mashu-HMI Mouse EST Project

JOURNAL Unpublished (1996)

COMMENT Contact: Marra M/Mouse EST Project
Mashu-HMI Mouse EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouse@est.wustl.edu
This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:503921
Seq primer: -28ml3 rev2 ER from Amersham
High quality sequence stop: 196.
Location/Qualifiers
1. .630
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone_image="851769"
/clone_id="Soares_mammary_gland_NbMNG"
/sex="male"
/tissue_type="mammary gland"
/dev_stage="4 weeks"
/lab_host="DH10B"
/note="Organ: mammary gland; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - 01190(df) primer [5].
TGTACCAATCTGTAAGTGGAGCGCGCGCAATGTTTTTTTTTTTTTTTTTTTTT
T 3'; double-stranded cDNA was ligated to Eco RI
adaptors (Pharmacia), digested with Not I and cloned into
the Not I and Eco RI sites of the modified pT73 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M.Fatima
Bonaldo."

BASE COUNT 144 a 196 c 152 g 138 t

ORIGIN

Query Match 26.7%; Score 282; DB 9; Length 630;
Best Local Similarity 69.0%; Pred. No. 6.2e-40;
Matches 436; Conservative 0; Mismatches 180; Indels 16; Gaps 3;

QY 210 ccgtgcggcgcggtcttacaagcagtggtcagctccaagcgtgtgcaagccctgcagc 269
|||||

Db 9 CAGGGGTGAGACTGCTTCTACAAATGAGCTGCAATTAATGATACCTGGCAGCAGTGTACA 68
|||||

QY 270 tgggttaacctagaagatggaggtgaagcagcgtgtgtgcaagggccacaagaagaca 329
|||||

Db 69 CAGTCAACCATCATGAGAGTGAAGTGAATCAACGACGAATTTGACACACTGATGAGATGCT 128
|||||

QY 330 gttctccgttcggcgcgccacccagccctggg-----cagctacaagcctgaggt 383
|||||

Db 129 GCTGTGACATGTAGACACGACGCCACCACTCGGCAAGAGCGGCTTACAGCTTGGAGTT 188
|||||

QY 384 gactgtccccctgcctcccaaggcactcttcccaagcgacacacacagcgtgtgcaagcc 443
|||||

Db 189 GACTGTGTTCCCTGCGCTCTGCGACACTTCTCCAGGACACACCCAGGCTGTGCAAGGCC 248
|||||

JOURNAL
COMMENT

Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabs-r@mail.nih.gov
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 cDNA Library Preparation: M. Bento Soares, Ph.D.
 cDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/bdrp/image/image.html
 Insert Length: 373 Std Error: 0.00
 Seq primer: -400P from GIBCO.
 Location/Qualifiers
 1..247

FEATURES
source

/organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:237536"
 /clone_1id="NCI-CGAP-Lu24"
 /tissue_type="carcinoid"
 /lab_host="DH10B"
 /note="Organ: lung; Vector: pT7R3D-Pac (Pharmacia) with a
 modified polylinker; Plasmid DNA from the normalized
 library NCI-CGAP_Lu5 was prepared, and ss circles were
 made in vitro. Following HAP purification, this DNA was
 used as tracer in a subtractive hybridization reaction.
 The driver was PCR-amplified cDNAs from a pool of 5,000
 clones made from the same library (clonoids
 1414920-1417991 and 1520904-1522439). Subtraction by Bento
 Soares and M. Fatima Bonaldo."

BASE COUNT
ORIGIN

41 a 70 c 79 g 57 t

Query Match

19.5%: Score 206.4; DB 9; Length 247;

Best Local Similarity 96.9%: Pred. No. 9.1e-27; Mismatches 6; Indels 1; Gaps 1;

Matches 221; Conservative 0; Indels 1; Gaps 1;

QY 831 accctggccaagatctgaccttgagcccaagaagtgaagctgggcccgcgccaagctgg 890
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 247 ACCCTGGCCAGATTGTGACC-TGGGCCCCACCAAGGTGAGCGCTGGGCCCCGCCAGCTGG 189
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 891 agcccgagaggtctgctggcgagcaaggagtgcaaggccgctgcccgcgcaagctcc 950
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 188 AGCCCGGAGGGTTGCTGGGGCAGCAGGAGGTGACAGCGCCGCTGCCGCCACAGCTCC 129
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 951 tgggccaactctgacggttctaagtgccgagtgtgctcgcgtctctcttaagtat 1010
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 128 TGGGCCAAGCTTTGACGCTTTAGTGCCGATGGCTGCTCAGGCTCTGTGCTTACGTAT 69
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1011 gcaatgatactctctgcccgcgagaccacaataaaaccttgagcag 1058
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 68 GCCATGCTACTCTCTGCCCCGCGGAGCCCAATATAAAACCTTGGCAG 21
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Search completed: June 18, 2002, 17:56:27
 Job time: 12105 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

Om nucleic - nucleic search, using sw model

```
Run on:      June 18, 2002, 14:34:42 ; Search time 285.57 Seconds
              (without alignments)
              6360.946 Million cell updates/sec
```

```

Title:      US-09-852-845-1
Perfect score: 1058
Sequence:   1 cagcagagcagagatgtgc.....cacataaaaccttgscag 1058

```

Gapop 10.0 , Gapext 1.0

```
Searched:      1736436 seqs, 858457221 residues
Total number of hits satisfying chosen parameters: 3472872
```

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

```
Post-processing: Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries
```

```
Database :
1: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT.*
2: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT.*
3: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT.*
4: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT.*
5: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1984.DAT.*
6: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT.*
7: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT.*
8: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT.*
9: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT.*
10: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT.*
11: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT.*
12: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT.*
13: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1992.DAT.*
14: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT.*
15: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT.*
16: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT.*
17: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT.*
18: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT.*
19: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT.*
20: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT.*
21: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT.*
22: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001.DAT.*
23: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.*
24: /net/abss06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2003.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	1044.4	98.7	1057	16	AA088758	ACT-4 cell surface
2	1044.4	98.7	1057	16	AA0704048	ACT-4-h-1 receptor
3	802	75.8	834	16	AA093257	Human OX-40 CDNA.
4	286.6	27.1	1317	16	AA070829	Plasmid pDC406/Ox4
5	286.6	27.1	1317	16	AAV32636	OX40/Fc cDNA.
6	283.2	26.8	618	16	AA070826	Mouse type-II memb
7	283.2	26.8	618	19	AAV32640	Mouse OX40 extrac
8	124.4	11.8	6080	22	AA546582	Tumour suppressor
9	111.2	10.5	117	22	AAH24887	Oligonucleotide fo

C	10	111.2	10.5	117	22	AAH24478	Human secondary si
C	11	111.2	10.5	117	22	AAH24544	Human secondary si
C	12	109.4	10.3	117	22	AAH24886	Oligonucleotide fo
C	13	109.4	10.3	117	22	AAH24477	Human secondary si
C	14	109.4	10.3	117	22	AAH24543	Human secondary si
C	15	108.6	10.3	6080	22	AAH24581	Tumour suppressor
C	16	101.6	9.6	5148	22	AAH24585	Tumour suppressor
C	17	79.8	7.5	5148	22	AAH24586	Tumour suppressor
C	18	67.6	6.4	11455	20	AAH53491	Human adenosine A1
C	19	59.6	5.6	114955	20	AAH53491	Human adenosine A1
C	20	56	5.3	763	21	AAZ45948	Human molecule ass
C	21	56	5.3	813	21	AAH58588	DNA encoding tumou
C	22	56	5.3	983	21	AAH50304	Human tumour necro
C	23	56	5.3	983	21	AAZ37762	Tumour necrosis fa
C	24	56	5.3	1006	19	AAV19153	Nucleotide sequenc
C	25	56	5.3	1007	21	AAH50303	Human tumour necro
C	26	56	5.3	1007	21	AAZ37763	TR1SLV1 nucleotid
C	27	56	5.3	1008	20	AAH87670	Human TNF receptor
C	28	56	5.3	1008	21	AAH99903	CDNA encoding huma
C	29	56	5.3	1008	21	AAH58595	Human PRO364 prote
C	30	56	5.3	1008	21	AAH77604	Human PRO364 CDNA
C	31	56	5.3	1008	21	AAH01240	Human PRO364 prote
C	32	56	5.3	1008	22	AAH85947	Native sequence o
C	33	56	5.3	1008	22	AAH85433	Clone DNA47365-12
C	34	56	5.3	1008	22	AAH30057	Human CDNA encodin
C	35	56	5.3	1008	22	AAH90566	Human PRO364 CDNA
C	36	56	5.3	1008	22	AAH91469	Human PRO364 CDNA
C	37	56	5.3	1008	22	AAH97479	Human angiogenesi
C	38	56	5.3	1074	21	AAH50306	Human tumour necro
C	39	56	5.3	1074	21	AAH237764	TR1SLV2 nucleotid
C	40	56	5.3	12425	22	AAH26495	Human low density
C	41	55.2	5.2	900	21	AAH53209	Monkey Fas ligand
C	42	53.4	5.0	1614	22	AAH26499	Human low density
C	43	52.6	5.0	125401	22	AAH17186	Streptomyces nours
C	44	51.6	5.0	3306	11	AAH05620	Expressible sequen
C	45	51.6	4.9	8459	22	AAH89557	Human histone deac

ALIGNMENTS

RESULT	1
AAQ08758	
ID	AAQ08758 standard; CDNA; 1057 BP.
AC	AAQ08758;
DT	21-NOV-1995 (first entry)
DE	ACT-4 cell surface receptor cDNA sequence.
XX	
XX	Cell surface receptor; ACT-4; T-lymphocyte; T-cell; Immune system
XX	ss.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
FT	CDS
FT	15..845
FT	/*tag= a
FT	15..86
FT	/*tag= b
FT	1042..1047
FT	polyA_site
FT	/*tag= c
XX	
XX	WO9512673-A.
XX	
PD	11-MAY-1995.
XX	
PE	03-NOV-1994;
XX	94WO-CB02415.
XX	
PR	03-NOV-1993;
XX	93US-0147784.
XX	
PA	(BECT) BECTON DICKINSON CO.

PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX Buck DW, Engleman EG, Godfrey W;
 XX WPI: 1995-18577/24.
 DR P-PSDB; AAR74737.
 XX
 XX Isolated ACT-4 receptor from activated T-cells - also its ligands and
 PT antibodies, useful for treating diseases of the immune system
 XX
 PS Claim 1; Fig. 5; 82pp; English.
 CC This sequence encodes the full-length cell surface receptor ACT-4
 CC isolated from activated CD4+ T-lymphocytes. The sequence may be
 CC expressed in e.g. COS-7 cells. The encoded protein, its ligands or
 CC fragments, and antibodies may be used for the treatment of transplant
 CC rejection, graft-versus-host disease, autoimmune disease, etc.
 XX
 SQ Sequence 1057 BP; 176 A; 390 C; 344 G; 147 T; 0 other;

Query Match 98.7%; Score 1044.4; DB 16; Length 1057;
 Best Local Similarity 99.8%; Pred. No. 4.2e-181;
 Matches 1056; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 cagcagaagacggagatgtctgtggggtcggcgctggcgcgggcgctgtgcgctc 60
 DB 1 cagcagaagacggagatgtctgtggggtcggcgctggcgcgggcgctgtgcgctc 60
 QY 61 tgcctctctctggcggtggggcgtgagcaacggtgacggggtcctactgtgtcggggaacct 120
 DB 61 tgcctctctctggcggtggggcgtgagcaacggtgacggggtcctactgtgtcggggaacct 120
 QY 121 acccagacgaacgacgggtgtctgacagtgacagccaggaacggatgtgtgacgct 180
 DB 121 acccagacgaacgacgggtgtctgacagtgacagccaggaacggatgtgtgacgct 180
 QY 181 gtagcgcgtcccaagaacaaagtggtcgctcgctggcgcggtcttctcaacgacgtgg 240
 DB 181 gtagcgcgtcccaagaacaaagtggtcgctcgctggcgcggtcttctcaacgacgtgg 240
 QY 241 tcagctccaagcgtgcaagccctgacagctgggttaacctcagaagtggaatgagcgga 300
 DB 241 tcagctccaagcgtgcaagccctgacagctgggttaacctcagaagtggaatgagcgga 300
 QY 301 agcagctgtgacagccacacaggaacagctctgcgctgcggcgggcgacccagcccc 360
 DB 301 agcagctgtgacagccacacaggaacagctctgcgctgcggcgggcgacccagcccc 360
 QY 361 tggagacgacaaagcctggaagtgtgactgtgccccctgacctcagaagggacattctccag 420
 DB 361 tggagacgacaaagcctggaagtgtgactgtgccccctgacctcagaagggacattctccag 420
 QY 421 ggcacaacacagcctgcaagccctggaacacttgcaacttgctggtggaacacacctgc 480
 DB 421 ggcacaacacagcctgcaagccctggaacacttgcaacttgctggtggaacacacctgc 480
 QY 481 agcgcggcagcaatagtctggaacaaatctgtgaggaacaggaacccccagcaacgacg 540
 DB 481 agcgcggcagcaatagtctggaacaaatctgtgaggaacaggaacccccagcaacgacg 540
 QY 541 cccagagagacccagggcccccgccagggccacatcactgtccagcccatgaaacctggcg 600
 DB 541 cccagagagacccagggcccccgccagggccacatcactgtccagcccatgaaacctggcg 600
 QY 601 ccagaaccccaagagacccctcaacccggcccggtggaagtgtcccgaggggcgctgcggtg 660
 DB 601 ccagaaccccaagagacccctcaacccggcccggtggaagtgtcccgaggggcgctgcggtg 660
 QY 661 ccgcatctctgggctgtggcctgt 720
 DB 661 ccgcatctctgggctgtggcctgt 720

QY 721 cctctgactgtctcggaggagacgaaggtgcgcccgatgcccacaaagccccctgggg 780
 DB 721 cctctgactgtctcggaggagacgaaggtgcgcccgatgcccacaaagccccctgggg 780
 QY 781 gaggcagttctcggaaccccatccaaagagagcagggcagccctcaccacttgagca 840
 DB 781 gaggcagttctcggaaccccatccaaagagagcagggcagccctcaccacttgagca 840
 QY 841 agatctgaccttgggcccccaaggtgagcgtcggcccccgccagagctggaagccggagg 900
 DB 841 agatctgaccttgggcccccaaggtgagcgtcggcccccgccagagctggaagccggagg 900
 QY 901 gctctgtggcagcagggcaggtgcaagcgctgcgcccgcaagctcctgtggccaact 960
 DB 901 gctctgtggcagcagggcaggtgcaagcgctgcgcccgcaagctcctgtggccaact 960
 QY 961 ctgcaacggttctaggtgacgaatgagcgtcctcggcctctgtcttaagtagtgcacatg 1020
 DB 961 ctgcaacggttctaggtgacgaatgagcgtcctcggcctctgtcttaagtagtgcacatg 1020
 QY 1021 cctctgtcccgcgggaccacataaanaaccttggcag 1057
 DB 1020 cctctgtcccgcgggaccacataaanaaccttggcag 1057

RESULT 2

AAT04048
 ID AAT04048 standard; CDNA; 1057 BP.
 XX
 AC AAT04048;
 XX
 DT 05-MAR-1996 (first entry)
 XX
 DE ACT-4-h-1 receptor cDNA sequence.
 XX
 KW ACT-4; specific binding partner; sbd; B cells; lymphocyte; GVHD;
 KW graft versus host disease; immune response; transplantation;
 KW autoimmune disease; inflammation; HIV; human immunodeficiency virus;
 KW HTLV; human T lymphocyte virus; inflammatory bowel disease;
 KW screening; identification; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 15..849
 FT /*tag= a
 FT /product= ACT-4-h-1 receptor.
 FT sig_peptide 15..86
 FT /*tag= b
 FT mat_peptide 87..846
 FT /*tag= c
 FT polyA_site 1042..1048
 FT /*tag= d
 XX
 XX W09521915-A1.
 XX
 XX 17-AUG-1995.
 XX
 XX 06-FEB-1995; 95WO-GB00238.
 XX
 XX 10-FEB-1994; 94US-0195967.
 XX
 PA (GREA/) GREAVES C P.
 PA (STRD) UNIV LELAND STANFORD JUNIOR.
 XX
 XX Engleman EG, Godfrey W;
 XX WPI: 1995-293117/38.
 DR P-PSDB; AAR79904.
 XX
 PT Ligand, ACT-4-1, to receptor on activated CD4 positive cells
 XX useful in treatment of various immune diseases and conditions

CC Then the murine OX-40 cDNA was used to probe a cDNA lambda gt11
CC library from human activated T lymphocytes to obtain human OX-40
CC cDNA. The published patent application states that the OX-40 cDNA
CC sequence is also in SQ ID no. 1, but this sequence is not present
CC in the spec. A nucleic acid having the sequence in SQ ID no 1 and
CC the polypeptide encoded by it are claimed.

XX Sequence 834 BP; 144 A; 298 C; 270 G; 122 T; 0 other;

Query Match 75.8%; Score 802; DB 16; Length 834;
Best Local Similarity 97.6%; Pred. No. 4.2e-137;
Matches 814; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

OY 15 atgtcgttggggggtcgcgcgtggtggcgccggcgctgtgcgtctctcctctgggc 74
DB 1 atgtcgttggggggtcgcgcgtggtggcgccggcgctgtgcgtctctcctctgggc 60
OY 75 ctgggggttgagacacgttgacgggggtctccactgtctgggggaacctaccacgaacgac 134
DB 61 ctgggggttgagacacgttgacgggggtctccactgtctgggggaacctaccacgaacgac 120
OY 135 cggctgtgcacagatgacagcgacgacgaagatgtgtagccgctgcagccgctccag 194
DB 121 cggctgtgcacagatgacagcgacgacgaagatgtgtagccgctgcagccgctccag 180
OY 195 aacacggtgtgcgtcgtctgcggcgccggtctctacacgaacgtgtgtcaagctcaagcgcg 254
DB 181 aacacggtgtgcgtcgtctgcggcgccggtctctacacgaacgtgtgtcaagctcaagcgcg 240
OY 255 tgcagaagcctgcacgttggtgttaacctcaagaatgtggagtgagcgagagagctgtgcag 314
DB 241 tgcagaagcctgcacgttggtgttaacctcaagaatgtggagtgagcgagagagctgtgcag 300
OY 315 gccacacagaagacacagctgtcgcgtctgcggcgccacccctgtgcacagctacaag 374
DB 301 gccacacagaagacacagctgtcgcgtctgcggcgccacccctgtgcacagctacaag 360
OY 375 ccttgagtgatgactgtgccccctgcctcagaagcaacttctccacggagacacacggcc 434
DB 361 ccttgagtgatgactgtgccccctgcctcagaagcaacttctccacggagacacacggcc 420
OY 435 tgcagaagcctgcacacacgtcgtgtgtgggaagcacacctgtgcagccgacgaacat 494
DB 421 tgcagaagcctgcacacacgtcgtgtgtgggaagcacacctgtgcagccgacgaacat 480
OY 495 agctcggagcgaactctgttgaagacagggacccccccagccacgacgacccagagacag 554
DB 481 agctcggagcgaactctgttgaagacagggacccccccagccacgacgacccagagacag 540
OY 555 ggcctcccgccagggcccatctctcagccacgtgaagcctgtgcagccacgaactcacg 614
DB 541 ggcctcccgccagggcccatctctcagccacgtgaagcctgtgcagccacgaactcacg 600
OY 615 ggaacctcaccacggccgttgaggtgcccgggggcgcggtgtgcacacatctctgggc 674
DB 601 ggaacctcaccacggccgttgaggtgcccgggggcgcggtgtgtgcacacatctctgggc 660
OY 675 ctgggacctgtgtctgggggtctgtggccccctgtgcacatctgtgccccctgtactgtc 734
DB 661 ctgggacctgtgtctgggggtctgtggccccctgtgcacatctgtgccccctgtactgtc 720
OY 735 cggagaggaacaaagactgtgcccccgatgcccacaagccccctggggggaagcaggttccgg 794
DB 721 cggagaggaacaaagactgtgcccccgatgcccacaagccccctggggggaagcaggttccgg 780
OY 795 acccccatcagaagagagcagcgacgacccactccacctgtgcagaagtctga 848
DB 781 acccccatcagaagagagcagcgacgacccactccacctgtgtcaagtctga 834

RESULT 4
AA00829

ID AAT00829 standard; cDNA; 1317 BP.
XX
XX AAT00829;
AC
XX
XX 30-MAR-1996 (first entry)
DT
XX
XX Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.
DE
XX
XX OX40; OX40-L; cytokine; cell surface molecule; plasmid;
KW pDC406/OX40/Fc*; membrane glycoprotein; ss.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..1317
FT /*tag- a
PN
XX US5457035-A.
XX
XX 10-OCT-1995.
PD
XX
XX 23-JUL-1993; 93US-0097827.
PF
XX
XX 23-JUL-1993; 93US-0097827.
PR
XX 23-JUL-1993; 93US-0097827.
XX
XX (IMMUNEX CORP.
PA
XX
XX Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
PI WPI; 1995-357992/46.
DR P-PSDB; AAR81882.
XX
XX New isolated DNA encoding the OX40 ligand polypeptide - also vectors
PT and host cells, used to produce recombinant ligand used in e.g.
PT prim. T cell culture, to modulate immune response etc.
XX
XX Example 2; Column 35-38; 26pp; English.
XX
XX This plasmid encodes an OX40/Fc antibody fragment mutein protein,
CC and is used to express a soluble OX40/Fc mutein fusion protein for
CC use in detecting CDNA clones encoding a OX40 ligand. The Fc
CC fragment may be derived from human IgG1, and the plasmid may be
CC used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell
CC line. Culture supernatant was purified by affinity chromatography
CC and this was used, together with labeled goat anti-human IgG to
CC screen various cell lines.
XX
SQ Sequence 1317 BP; 322 A; 417 C; 337 G; 241 T; 0 other;

Query Match 27.1%; Score 286.6; DB 16; Length 1317;
Best Local Similarity 66.6%; Pred. No. 1.5e-43;
Matches 428; Conservative 0; Mismatches 209; Indels 6; Gaps 1;

OY 87 accgtgacgggggtccactgtgtcgggggacactaccacgaacgacggtgtgtccac 146
DB 61 accgtgacgggggtccactgtgtcgggggacactaccacgaacgacggtgtgtcgt 120
OY 147 gagtgacggcgaagcaacggagtggtgacgctgtgacgcgtccacgaacagtgctgc 206
DB 121 gagtgacggcgaagcaacggagtggtgacgctgtgacgcgtccacgaacagtgctgc 180
OY 207 cgttcgtggggcggtctctacacgacggtgtgtagctccacgaacggcgtgc 266
DB 181 cgttcgtggagactgtgtctctacacgacggtgtgtagctccacgaacggcgtgc 240
OY 267 acgtgtgttaacctcagaagtggtgagcggaaacagctgtgcacggccacacagggac 326
DB 241 acacagtgcaacatcgaagtgtgaaagttaactcaagcagaatgtgcacactactcggat 300
OY 327 acagtgctgcgtcgtggcgacccacgacccctgtga-----cagctacaagcctga 380
DB 301 actgtctgcagatgtagaccagggacccacacccctgcgacgagacgctacagcctga 360

QY 381 gttgactgtgccccctgcccctccagggcacttctcccaaggcgaacaggcctgcaag 440
D 361 gttagctgtgtccctgcccctccctgcccacttctccaggaacaacaggcctgcaag 420
QY 441 ccctggaaccaactgcactgtgtggaagacacaccctgcagccgagcaaatgtcg 500
D 421 cccctggaaccaactgtactatcttgaaagacagaccgcacccagcagtgacagtctg 480
QY 501 gaccgaatctgtggaaggagagagagagagagagagagagagagagagagagagag 560
D 481 gaccgaatctgtggaaggagagagagagagagagagagagagagagagagagagag 540
QY 561 ccggcagagcccatcactgtccagcccaactgaagcctgtgcccagagaagagagagag 620
D 541 acattcagagcccaactcactgtcccaactcaccacagctgtgcccagagacttgcagtgc 600
QY 621 tcaacccgagccgtggaaggtcccccgggggagcgtgcggtgcgcacatccctggcctgg 680
D 601 tctaacaccacactgtgtggaagccagatctgtgacaacaactcacacatgcccacgtgc 660
QY 681 ctgtgtcgtgggctgtgagcccccctgtgcccactcctgctgagcc 723
D 661 ccagcactgaagcagagagcgcgctcagcttccctcc 703

RESULT 5

AAV32636
ID AAV32636 standard; cDNA to mRNA; 1317 BP.
XX AAV32636;
AC
DT 25-SEP-1998 (first entry)
XX
DE OX40/Fc CDNA.
XX
KM OX40/Fc; cytokine; T cell antigen; TH-2 immune response; OX40-L;
KW chimeric; ss.
XX
OS Synthetic.
OS Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 1..1317
FT /tag= b
FT product= "OX40/Fc mutein"
FT 1..618
FT /tag= a
FT /note= "encodes mouse OX40 extracellular domain"
FT 619..1314
FT /tag= b
FT /note= "encodes mutant Fc region of human IgG1"
FT 673..675
FT /tag= c
FT /note= "changed from CTC in wild-type to GCC in mutant"
FT 676..678
FT /tag= d
FT /note= "changed from CTG in wild-type to GAG in mutant"
FT mutation
FT 682..684
FT /tag= e
FT /note= "changed from GGA in wild-type to GCG in mutant"
XX
PN US5783665-A.
XX
XX 21-JUL-1998.
PD
XX 22-JUN-1995; 95US-0494574.
PF
XX 23-JUL-1993; 93US-0097827.

PR 22-JUN-1995; 95US-0494574.
XX
XX (IMM) IMMUNEX CORP.
PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
PI WPI; 1998-427099/36.
DR P-PSDB; AAM48976.
XX
XX Purified polypeptide OX-40 ligands - for co-stimulation of T-cell
PT production and binding assays for OX-40 and homologues
PS
PS Example 2; Col 35-38; 26pp; English.
CC The present sequence represents the OX40/Fc cDNA which encodes a
CC fusion protein that contains the extracellular domain of mouse OX40
CC fused to the mutated Fc region of the human IgG1 antibody. The
CC fusion protein was used for detecting cDNA clones encoding an OX40
CC ligand. The invention claims for a murine OX40-L cytokine (AAM48975)
CC that binds to the murine T cell antigen, OX40. The OX40-L protein
CC is claimed to be useful for co-stimulation of T-cell production and
CC in binding assays for detecting OX40 or its homologues. The OX40-L
CC protein is also claimed to generate a TH-2 immune response.
SO Sequence 1317 BP; 322 A; 417 C; 337 G; 241 T; 0 other;

Query Match 27.1%; Score 286.6; DB 19; Length 1317;
Best Local Similarity 66.6%; Pred. No. 1.5e-43;
Matches 428; Conservative 0; Mismatches 209; Indels 6; Gaps 1;

QY 87 accgtgacggggcctcactgtgtcgggagacactaccacagcagaccggtgtgtccac 146
D 61 acagcaaggcggctcactgtgttaactactactaccacagcgtgtgtgtgtgtgt 120
QY 147 gaggtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 206
D 121 gaggtagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 180
QY 207 cgtccgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 266
D 181 catccgtgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 240
QY 267 acgtgtgtaacctcagaaagtgtgagtgagcagcagcagcagcagcagcagcagcagc 326
D 241 acacagtgtaacctcagaaagtgtgagtgagcagcagcagcagcagcagcagcagcagc 300
QY 327 acagtcgtgcgtgtgcgggagcagcagcagcagcagcagcagcagcagcagcagcagc 380
D 301 actgtctgagatgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
QY 381 gttgactgtgccccctgcccctccaggaacttctccagggagaaacaggcctgtgcaag 440
D 361 gttagctgtgtccctgcccctccctgcccacttctccaggaacacaggcctgtgcaag 420
QY 441 ccctggaaccaactgcactgtgtggaagacacaccctgaagccgagcagcaatagtctcg 500
D 421 cccctggaaccaatgtactatcttgaaagacagaccgcacccagcagtgacagtctg 480
QY 501 gaccgaatctgtggaaggagagagagagagagagagagagagagagagagagagag 560
D 481 gaccgaatctgtggaaggagagagagagagagagagagagagagagagagagagag 540
QY 561 ccggcagagcccatcactgtccagcccaactgaagcctgtgcccagagaagcagagagag 620
D 541 acattcagagcccaactcactgtcccaactcaccacagctgtgcccagagacttgcagtgc 600
QY 621 tcaacccgagccgtggaaggtcccccgggggagcgtgcggtgcgcacatccctggcctgg 680
D 601 tctaacaccacactgtgtggaagccagatctgtgacaacaactcacacatgcccacgtgc 660
QY 681 ctgtgtcgtgggctgtgagcccccctgtgcccactcctgctgagcc 723

Db 661 ccagcactgaagccgagggcgccgctcagctctctctcc 703

RESULT 6
AA00826
ID AAT00826 standard; CDNA to mRNA; 618 BP.
AC AAT00826;
XX
XX
XX 30-MAR-1996 (first entry)
XX
XX Mouse type-II membrane polypeptide OX40 extracellular domain.
DE
XX OX40; OX40-L; cytokine; cell surface molecule;
KM membrane glycoprotein; ss.
XX
XX Mus musculus.
OS
XX US5457035-A.
XX
XX 10-OCT-1995.
PD
XX 23-JUL-1993; 93US-0097827.
XX
XX 23-JUL-1993; 93US-0097827.
XX
XX 23-JUL-1993; 93US-0097827.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
XX
XX WPI: 1995-357992/46.
XX
XX P-PSDB; AAR81881.
XX
XX New isolated DNA encoding the OX40 ligand polypeptide - also vectors
XX
XX PT and host cells, used to produce recombinant ligand used in e.g.
XX
XX PT prim. T cell culture, to modulate immune response etc.
XX
XX PS Example 1; Column 31-32; 26pp; English.
XX
XX CC This sequence encodes the extracellular domain of OX40, a membrane
XX
XX CC glycoprotein present on the CD4 positive subset of activated T
XX
XX CC cells.
XX
XX SO Sequence 618 BP; 148 A; 187 C; 151 G; 132 T; 0 other;

Query Match 26.8%; Score 283.2; DB 16; Length 618;
Best Local Similarity 70.6%; Pred. No. 6.4e-43;
Matches 394; Conservative 0; Mismatches 158; Indels 6; Gaps 1;

Qy 87 accgtagcggtctcactgtgtcggtgacacacccacgaacgacggtgtgtcac 146
Db 61 acagcagcgcggtcactgtgtttaaatacaccacccaggtgtgtgtgtgt 120
Qy 147 gagtcagggccgagcagggaggtgtgtgagccgctgacagcggtgtgtgtc 206
Db 121 gagtgcagccagcgacaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 180
Qy 207 cgtccgtgcggcggtcttactaacagcgtgtgtcagctcccaagcggtgtgtc 266
Db 181 catccgtgtgagactgtcttactaacatgaagctgtcgaattatgatacctgtgtg 240
Qy 267 acgtgtgttaactcagaaggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 326
Db 241 acacagctcacaacatcgaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 300
Qy 327 acagctcgcgt 380
Db 301 actgtctcgt 360
Qy 381 gttgactgt 440
Db 361 gttgactgt 420

Qy 441 cccgtgaccactgtcacctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 500
Db 421 cccgtgaccactgt 480
Qy 501 gacgcactgt 560
Db 481 gacgcactgt 540
Qy 561 ccggccagggccatcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 620
Db 541 acattcagggccacacactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 600
Qy 621 tccaccggccgt 638
Db 601 tctacaccactgt 618

RESULT 7
AAV32640
ID AAV32640 standard; CDNA to mRNA; 618 BP.
XX
XX AAV32640;
AC
XX 25-SEP-1998 (first entry)
XX
XX Mouse OX40 extracellular domain encoding CDNA.
DE
XX OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L;
KM OX40/Fc; ss.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH 1. 618
FT CDS
FT
FT /product= "Mouse OX40 extracellular region"
FT /note= "CDS does not contain a stop codon"

US5783665-A.
21-JUL-1998.
22-JUN-1995; 95US-0494574.
23-JUL-1993; 93US-0097827.
PR 22-JUN-1995; 95US-0494574.
XX
XX (IMMV) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
XX
XX WPI: 1998-427099/36.
XX
XX P-PSDB; AAW48977.
XX
XX Purified polypeptide OX-40 ligands - for co-stimulation of T-cell
XX
XX PT production and binding assays for OX-40 and homologues
XX
XX PS Example 1; Col 31-32; 26pp; English.
XX
XX CC The present sequence represents the mouse OX40 extracellular domain
XX
XX CC encoding CDNA. The extracellular domain of OX40 is its ligand
XX
XX CC binding domain. The present CDNA was used in the construction of the
XX
XX CC chimeric OX40/Fc CDNA (AAV32640). The invention claims for a murine
XX
XX CC OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen.
XX
XX CC The OX40-L protein is claimed to be useful for co-stimulation of
XX
XX CC T-cell production and in binding assays for detecting OX40 or its
XX
XX CC homologues. The OX40-L protein is also claimed to generate a TH-2
XX
XX CC immune response.
XX
XX SO Sequence 618 BP; 148 A; 187 C; 151 G; 132 T; 0 other;

XX Stimulatory primary signalling motif; immune cell; signal transduction;
KW chimeric receptor; inflammatory disease; autoimmune disease; asthma;
KW eczema; congenital disease; cystic fibrosis; sickle cell anemia;
KW dermatological disease; psoriasis; neurological disease;
KW multiple sclerosis; transplant-related disease; metabolic disease;
KW organ transplant rejection; graft versus host disease;
KW idiopathic disease; diabetes; cancer; ss.
OS Synthetic.
XX
XX WO200132709-A2.
XX
XX 10-MAY-2001.
XX
XX 01-NOV-2000; 2000WO-GB04183.
XX
XX 01-NOV-1999; 99GB-0025848.
XX
XX (CELL-) CELLTech CHIROSCIENCE LTD.
XX
XX Finney HM, Lawson ADG;
XX
XX WPI; 2001-389718/41.
XX
XX Novel cytoplasmic signalling protein and chimeric receptor protein,
PT useful for treating HIV infection, asthma, eczema, psoriasis, multiple
PT sclerosis, contain non-natural stimulatory primary signalling motif -
XX
XX Example 2; Fig 3; 45pp; English.
XX
XX Oligonucleotides AAH2486-87 were used to construct DNA encoding
CC secondary signalling sequences. The specification describes stimulatory
CC primary signalling motifs. Primary motifs are efficient at at
CC mediating immune cell signal transduction, particularly when
CC incorporated in an intracellular signalling domain of a chimeric
CC receptor. The primary signalling motif can be combined in any way so
CC as to achieve the desired level of activation (or inhibition) of a
CC number of secondary messenger cascades. The signalling motifs are useful
CC in therapy and in the manufacture of medicament for treating or
CC preventing disease in humans or animals. They are useful for treating
CC human patients suffering from infectious diseases e.g. human
CC immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases
CC such as asthma and eczema, congenital diseases e.g. cystic fibrosis,
CC sickle cell anemia, dermatological diseases e.g. psoriasis, neurological
CC diseases e.g. multiple sclerosis, transplant-related disease e.g. organ
CC transplant rejection, graft versus host disease, metabolic/idiopathic
CC disease e.g. diabetes, and cancer.
XX
XX Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;
SO

Query Match 10.5%; Score 111.2; DB 22; Length 117;
Best Local Similarity 97.4%; Pred. No. 1.1e-11;
Matches 113; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 735 cggaggagaccagagctgcggcccgatgccacaagccccctggggagagcagttccgg 794
DB 116 CGAGGAGACCAAGAGCTGCCCGCCCGCAAAACCCCTGGGGAGAGCAGTTTCCCG 57
OY 795 acccccatcagaagagagcagcgagccgacctccacctggccaagatctgacc 850
DB 56 ACCCCCATCAAGAGAGAGGAGCGCCGACGCCACTCCACCTGCGCCAAAGATCGATC 1

RESULT 10
AAH24478/C
ID AAH24478 standard; DNA; 117 BP.
XX AAH24478;
XX
XX 07-AUG-2001 (first entry)
XX

DE Human secondary signalling motif SB34 oligo F1340B.
XX
XX Human: primary signalling motif; sequence block; SB; immunosuppressive;
KW secondary signalling sequence; antimicrobial; antiinflammatory;
KW dermatological; neuroprotective; cytostatic; anti-HIV; antistimatic;
KW antistickling; antipsoriatic; antidiabetic; gene therapy; diabetes;
KW immune cell signal transduction; infection; inflammation; cancer;
KW autoimmune disease; congenital disease; psoriasis; neurological disease;
KW organ transplant rejection; ss.
XX
XX Homo sapiens.
XX
XX WO200132867-A1.
XX
XX 10-MAY-2001.
XX
XX 01-NOV-2000; 2000WO-GB04193.
XX
XX 01-NOV-1999; 99GB-0025853.
XX
XX (CELL-) CELLTech CHIROSCIENCE LTD.
XX
XX Finney HM, Lawson ADG;
XX
XX WPI; 2001-328791/34.
XX
XX New nucleic acids encoding polypeptides with expanded primary signalling
PT motifs, for use in gene therapy, particularly for treating or
PT preventing infections, inflammations or autoimmune diseases in humans
XX
XX Example 2; Fig 3; 43pp; English.
XX
XX The invention relates to novel primary signalling motifs containing
CC a consensus amino acid sequence. These motifs are extremely
CC efficient at mediating immune cell signal transduction, particularly
CC when incorporated into an intracellular signalling domain of a chimeric
CC receptor. Nucleic acids that encode, and polypeptides that contain,
CC these primary signalling motifs are useful in medicine and research.
CC They are useful in therapy, or in the manufacture of a medicament for
CC treating or preventing disease in humans or in animals. These diseases
CC include infections (e.g. HIV (human immunodeficiency virus) infection),
CC inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital
CC diseases (e.g. cystic fibrosis or sickle cell anemia), dermatological
CC diseases (e.g. psoriasis), neurological diseases (e.g. multiple
CC sclerosis), organ transplant rejection or graft-versus-host disease, or
CC metabolic/idiopathic diseases (e.g. diabetes or cancer). The
CC present sequence is one of a large number of oligonucleotides used in
CC the construction of sequence blocks (SBS) of primary and secondary
CC signalling motifs. Primary signalling motifs are sequences that
CC transduce either a stimulatory or an inhibitory signal, which regulates
CC primary activation of the T cell receptor (TCR) complex. Secondary
CC motifs impart secondary or co-stimulatory signalling capacity to a
CC molecule in T cells.
XX
XX Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;
SO

Query Match 10.5%; Score 111.2; DB 22; Length 117;
Best Local Similarity 97.4%; Pred. No. 1.1e-11;
Matches 113; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 735 cggaggagaccagagctgcggcccgatgccacaagccccctggggagagcagttccgg 794
DB 116 CGAGGAGACCAAGAGCTGCCCGCCCGCAAAACCCCTGGGGAGAGCAGTTTCCCG 57
OY 795 acccccatcagaagagagcagcgagccgacctccacctggccaagatctgacc 850
DB 56 ACCCCCATCAAGAGAGAGGAGCGCCGACGCCACTCCACCTGCGCCAAAGATCGATC 1

RESULT 11
AAH24544/C

ID AAH24544 standard; DNA: 117 BP.
XX
AC AAH24544;
XX
DT 08-AUG-2001 (first entry)
XX
DE Human secondary signalling motif SB34 oligo F1340B.
XX
KW Human: anti-HIV; antiinflammatory; antistimatic; dermatological;
KW antisticking; antiporiatic; neuroprotective; immunosuppressive;
KW antidiabetic; cytosatic; HIV infection; inflammation;
KW autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;
KW neurological disease; organ transplant rejection; diabetes; cancer;
KW graft-versus-host disease; adaptor receptor protein; sequence block;
KW SB; primary signalling motif; secondary signalling motif; ss.
XX
OS Homo sapiens.
XX
PN MO200132866-A2.
XX
PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-GB04189.
XX
PR 01-NOV-1999; 99GB-0025854.
XX
PA (CELL-) CELLTRECH CHIROSCEINCE LTD.
XX
PI Finney HM, Lawson ADG;
XX
DR WPI: 2001-328790/34.
XX
PT Novel polynucleotide encoding adaptor receptor protein useful for
PT treating human immunodeficiency virus (HIV) infection, asthma, cystic
PT fibrosis, multiple sclerosis, organ transplant rejection, diabetes and
PT cancer.
XX
PS Example 3; Fig 3; 52pp; English.
XX
CC The invention relates to a novel nucleic acid encoding an adaptor
CC receptor protein comprising an extracellular ligand-binding domain, a
CC transmembrane domain and an intracellular signalling domain. The
CC intracellular signalling domain comprises the cytoplasmic portion of at
CC least one adaptor protein, and the extracellular ligand-binding domain
CC is not CD8 or a major histocompatibility complex (MHC) class I protein.
CC The adaptor receptor protein and the nucleic acid encoding it are useful
CC in therapy. They are useful in the manufacture of a medicament for the
CC treatment or prevention of disease in humans and animals. They are useful
CC in the treatment of infectious diseases (e.g. HIV infection),
CC inflammatory and autoimmune diseases (e.g. asthma and eczema),
CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia),
CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g.)
CC multiple sclerosis), organ transplant rejection, graft-versus-host
CC disease and metabolic/idiopathic diseases such as diabetes and cancer.
CC The present sequence is one of a large number of oligonucleotides used
CC in the construction of sequence blocks (SBS) of primary and secondary
CC signalling motifs. Primary signalling motifs transduce either a
CC stimulatory or an inhibitory signal, which regulates primary activation
CC of the T cell receptor (TCR) complex. Secondary signalling motifs impart
CC secondary or co-stimulatory signalling capacity to a molecule in T
CC cells. Primary and secondary signalling motifs may be used as
CC components of the adaptor receptor protein of the invention.
XX
SQ Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;

Query Match 10.5%; Score 111.2; DB 22; Length 117;
Best Local Similarity 97.4%; Pred. No. 1.1e-11;
Matches 113; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 735 cggagggaccagagctgccccccatgcccccaagccccccggggggagagcgttccgg 794
DB 116 CGGAGGACCAAGGCTGCCGCCGATGCCCAAAAGCCCCCGGGGAGGACAGTTTCCGG 57

QY 795 accccatccaagagagcgagccgacccactccaccctggccaagatcgacc 850
DB 56 ACCCCATCCAAAGAGGACGAGCCGACGCCCTCCACCTCGCCAAAGTCGGATC 1

RESULT 12
AAH24886
ID AAH24886 standard; DNA: 117 BP.
XX
AC AAH24886;
XX
DT 22-AUG-2001 (first entry)
XX
DE Oligonucleotide for a secondary signalling motif.
XX
KW Stimulatory primary signalling motif; immune cell; signal transduction;
KW chimeric receptor; inflammatory disease; autoimmune disease; asthma;
KW eczema; congenital disease; cystic fibrosis; sickle cell anemia;
KW dermatological disease; psoriasis; neurological disease;
KW multiple sclerosis; transplant-related disease; metabolic disease;
KW organ transplant rejection; graft versus host disease;
KW idiopathic disease; diabetes; cancer; ss.
XX
OS Synthetic.
XX
PN MO200132709-A2.
XX
PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-GB04183.
XX
PR 01-NOV-1999; 99GB-0025848.
XX
PA (CELL-) CELLTRECH CHIROSCEINCE LTD.
XX
PI Finney HM, Lawson ADG;
XX
DR WPI: 2001-389718/41.
XX
PT Novel cytoplasmic signalling protein and chimeric receptor protein,
PT useful for treating HIV infection, asthma, eczema, psoriasis, multiple
PT sclerosis, contain non-natural stimulatory primary signalling motif -
XX
PS Example 2; Fig 3; 45pp; English.
XX
CC Oligonucleotides AAH24886-87 were used to construct DNA encoding
CC secondary signalling sequences. The specification describes stimulatory
CC primary signalling motifs. Primary motifs are efficient at at
CC mediating immune cell signal transduction, particularly when
CC incorporated in an intracellular signalling domain of a chimeric
CC receptor. The primary signalling motif can be combined in any way so
CC as to achieve the desired level of activation (or inhibition) of a
CC number of secondary messenger cascades. The signalling motifs are useful
CC in therapy and in the manufacture of medicament for treating or
CC preventing disease in humans or animals. They are useful for treating
CC human patients suffering from infectious diseases e.g. human
CC immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases
CC such as asthma and eczema, congenital diseases e.g. cystic fibrosis,
CC sickle cell anemia, dermatological diseases e.g. psoriasis, neurological
CC diseases e.g. multiple sclerosis, transplant-related disease e.g. organ
CC transplant rejection, graft versus host disease, metabolic/idiopathic
CC disease e.g. diabetes, and cancer.
XX
SQ Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;

Query Match 10.3%; Score 109.4; DB 22; Length 117;
Best Local Similarity 99.1%; Pred. No. 2.3e-11;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 cggagggaccagagctgccccccatgcccccaagccccccggggggagagcgttccgg 794
DB 116 CGGAGGACCAAGGCTGCCGCCGATGCCCAAAAGCCCCCGGGGAGGACAGTTTCCGG 57

Db 6 cggaggaccagagctgcccccagatgccacaagcccccctggggaggcagttccgg 65
Oy 795 accccatccaagagagagcagcgccagccactccaccctggtccaagatc 845
|||||
Db 66 accccatccaagagagagcagcgccagccactccaccctggtccaagatc 116

RESULT 13

AAH24477
ID AAH24477 standard; DNA; 117 BP.

XX AAH24477;
AC

XX 07-AUG-2001 (first entry)
DT

XX Human secondary signalling motif SB34 oligo F1340A.
DE

XX Human; primary signalling motif; sequence block; SB; immunosuppressive;
KW secondary signalling sequence; antimicrobial; antiinflammatory;
KW dermatological; neuroprotective; cytostatic; anti-HIV; antidiabetic;
KW antislacking; antipsoriatic; antidiabetic; gene therapy; diabetes;
KW immune cell signal transduction; infection; inflammation; cancer;
KW autoimmune disease; congenital disease; psoriasis; neurological disease;
KW organ transplant rejection; ss.

XX Homo sapiens.
OS

XX WO200132867-A1.
PN

XX 10-MAY-2001.
PD

XX 01-NOV-2000; 2000WO-GB04193.
PF

XX 01-NOV-1999; 99GB-0025853.
PR

XX (CELL-) CELLTech CHIROSCIENCE LTD.
PA

XX Flinney HM, Lawson ADG;
PI

XX WPI; 2001-328791/34.
DR

XX New nucleic acids encoding polypeptides with expanded primary signalling
PT motifs, for use in gene therapy, particularly for treating or
PT preventing infections, inflammations or autoimmune diseases in humans
PT

XX Example 2; Fig 3; 43bp; English.
PS

XX The invention relates to novel primary signalling motifs containing
CC a consensus amino acid sequence. These motifs are extremely
CC efficient at mediating immune cell signal transduction, particularly
CC when incorporated into an intracellular signalling domain of a chimeric
CC receptor. Nucleic acids that encode, and polypeptides that contain,
CC these primary signalling motifs are useful in medicine and research.
CC They are useful in therapy, or in the manufacture of a medicament for
CC treating or preventing disease in humans or in animals. These diseases
CC include infections (e.g. HIV (human immunodeficiency virus) infection),
CC inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital
CC diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological
CC diseases (e.g. psoriasis), neurological diseases (e.g. multiple
CC sclerosis), organ transplant rejection or graft-versus-host disease, or
CC metabolic/idiopathic diseases (e.g. diabetes or cancer). The
CC present sequence is one of a large number of oligonucleotides used in
CC the construction of sequence blocks (SBS) of primary and secondary
CC signalling motifs. Primary signalling motifs are sequences that
CC transduce either a stimulatory or an inhibitory signal, which regulates
CC primary activation of the T cell receptor (TCR) complex. Secondary
CC motifs impart secondary or co-stimulatory signalling capacity to a
CC molecule in T cells.

XX Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;
SO

Query Match 10.3%; Score 109.4; DB 22; Length 117;
Best Local Similarity 99.1%; Pred. No. 2.3e-11;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 735 cggaggaccagagctgcccccagatgccacaagcccccctggggaggcagttccgg 794
|||||
Db 6 cggaggaccagagctgcccccagatgccacaagcccccctggggaggcagttccgg 65

Oy 795 accccatccaagagagagcagcgccagccactccaccctggtccaagatc 845
|||||
Db 66 accccatccaagagagagcagcgccagccactccaccctggtccaagatc 116

RESULT 14

AAH24543
ID AAH24543 standard; DNA; 117 BP.

XX AAH24543;
AC

XX 08-AUG-2001 (first entry)
DT

XX Human secondary signalling motif SB34 oligo F1340A.
DE

XX Human; anti-HIV; antiinflammatory; antislacking; dermatological;
KW antislacking; antipsoriatic; neuroprotective; immunosuppressive;
KW antidiabetic; cytostatic; HIV infection; inflammation;
KW autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;
KW neurological disease; organ transplant rejection; diabetes; cancer;
KW graft-versus-host disease; adaptor receptor protein; sequence block;
SB; primary signalling motif; secondary signalling motif; ss.

XX Homo sapiens.
OS

XX WO200132866-A2.
PN

XX 10-MAY-2001.
PD

XX 01-NOV-2000; 2000WO-GB04189.
PF

XX 01-NOV-1999; 99GB-0025854.
PR

XX (CELL-) CELLTech CHIROSCIENCE LTD.
PA

XX Flinney HM, Lawson ADG;
PI

XX WPI; 2001-328790/34.
DR

XX Novel polynucleotide encoding adaptor receptor protein useful for
PT treating human immunodeficiency virus (HIV) infection, asthma, cystic
PT fibrosis, multiple sclerosis, organ transplant rejection, diabetes and
PT cancer.

XX Example 3; Fig 3; 52bp; English.
PS

XX The invention relates to a novel nucleic acid encoding an adaptor
CC receptor protein comprising an extracellular ligand-binding domain, a
CC transmembrane domain and an intracellular signalling domain. The
CC intracellular signalling domain comprises the cytoplasmic portion of at
CC least one adaptor protein, and the extracellular ligand-binding domain
CC is not CD8 or a major histocompatibility complex (MHC) class I protein.
CC The adaptor receptor protein and the nucleic acid encoding it are useful
CC in therapy. They are useful in the manufacture of a medicament for the
CC treatment or prevention of disease in humans and animals. They are useful
CC in the treatment of infectious diseases (e.g. HIV infection),
CC inflammatory and autoimmune diseases (e.g. asthma and eczema),
CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia),
CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g.)
CC multiple sclerosis), organ transplant rejection, graft-versus-host
CC disease and metabolic/idiopathic diseases such as diabetes and cancer.
CC The present sequence is one of a large number of oligonucleotides used
CC in the construction of sequence blocks (SBS) of primary and secondary
CC signalling motifs. Primary signalling motifs transduce either a
CC stimulatory or an inhibitory signal, which regulates primary activation

CC of the T cell receptor (TCR) complex. Secondary signalling motifs impart
CC secondary or co-stimulatory signalling capacity to a molecule in T
CC cells. Primary and secondary signalling motifs may be used as
CC components of the adaptor receptor protein of the invention.
XX Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;

Query Match 10.3%; Score 109.4; DB 22; Length 117;
Best Local Similarity 99.1%; Pred. No. 2.3e-11;
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 cgaagagacacagagctgcccccgatgcccacaagccccctggggagagcagttccgg 794
|||||
Db 6 cgaagagacacagagctgcccccgatgcccacaagccccctggggagagcagttccgg 65

QY 795 accccatccaaagagagagcagcgacgcccacatccaccctggccaagatc 845
|||||
Db 66 accccatccaaagagagagcagcgacgcccacatccaccctggccaagatc 116

RESULT 15

IDS AAS46581 standard; DNA; 6080 BP.

XX AAS46581;

DT 18-DEC-2001 (first entry)

DE Tumour suppressor gene derived chemically modified sequence #303.

XX Human; tumour suppressor gene; oncogene; antitumour; cytosolic;

KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;

XX cytosine methylation; ds.

OS Homo sapiens.

XX WO200168912-A2.

XX 20-SEP-2001.

PD 15-MAR-2001; 2001WO-EP02955.

XX 15-MAR-2000; 2000DE-1013847.

PR 06-APR-2000; 2000DE-1019058.

PR 07-APR-2000; 2000DE-1019173.

PR 30-JUN-2000; 2000DE-1032529.

PR 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-602752/68.

XX Claim 1; SEQ ID NO 303; 27pp; English.

XX The invention relates to a nucleic acid comprising a sequence of 18

CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with

CC bisulphite, of genes associated with tumour suppression and

CC oncogenes having a sequence taken from 536 (actually 533 since

CC numbers 408, 458 and 500 are missing from the sequence listing) sequences

CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a

CC peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may

CC form part of a set of probes for detecting the cytosine methylation state

CC and/or single nucleotide polymorphisms and also to be used in an

CC array for analysing diseases associated with CpG dinucleotides e.g.

CC cancers and tumours. The probes can also be used in a method for

CC ascertaining genetic and/or epigenetic parameters for the diagnosis
CC and/or therapy of existing diseases or the predisposition to specific
CC diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes.

CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 6080 BP; 1015 A; 278 C; 1978 G; 2809 T; 0 other;

Query Match 10.3%; Score 108.8; DB 22; Length 6080;
Best Local Similarity 70.2%; Pred. No. 2.9e-11;
Matches 146; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 851 ttggcccccaaggtgacgctggcccccgccagagctggagcccgagggctgctgg 910
|||||

Db 19 ttgggttatataggtgacgctggggcttgcgttaagttggagttcgagggcttgg 78

QY 911 cgaagagagcaggtgacgagccgctgccccgccaagctctggccaactctgacagtt 970
|||||

Db 79 cgaagagagcaggtgacgagccgctgccccgccaagctctggccaactctgacagtt 138

QY 971 ctaggctccgagtgctgctcgcgctctgcttgcgtatgcatagcataactctctgcc 1030
|||||

Db 139 ttagggtgcagtgctgctcgcgctctgcttgcgtatgcatagcataactctctgcc 198

QY 1031 cgcgggaccacaataaaacctggcag 1058
|||||

Db 199 cgcgggattataataaaatttggtag 226

Search completed: June 18, 2002, 18:50:45
Job time: 15363 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:15:24 ; Search time 1824.31 Seconds
(without alignments)
12136.246 Million cell updates/sec

Title: US-09-852-845-1

Perfect score: 1058

Sequence: 1 cagcagagacgagagatgtgc.....cacataaaaccttgcag 1058

Scoring table: OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :

GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_om:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vi:*

15: em_ba:*

16: em_fun:*

17: em_hum:*

18: em_in:*

19: em_mu:*

20: em_om:*

21: em_or:*

22: em_ov:*

23: em_pat:*

24: em_ph:*

25: em_pl:*

26: em_ro:*

27: em_sts:*

28: em_un:*

29: em_vi:*

30: em_htg_hum:*

31: em_htg_inv:*

32: em_htg_other:*

33: em_htgo_inv:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description

1	886	83.7	1057	6	AR048669	AR048669 Sequence
2	886	83.7	1057	6	AR156875	AR156875 Sequence
3	831	78.5	1034	9	S76792	S76792 OX40-cell s
4	740	69.9	1373	9	HSROX40MR	X75962 H. sapiens m
5	207	19.6	5150	9	HSR277151	AU277151 Homo sapi
6	207	19.6	11119	2	AL162741	AL162741 Homo sapi
7	207	19.6	210944	2	AL1390719	AL1390719 Homo sapi
8	83	7.8	117	6	AX134865	AX134865 Sequence
9	83	7.8	117	6	AX134962	AX134962 Sequence
10	83	7.8	117	6	AX135075	AX135075 Sequence
11	78	7.4	117	6	AX134866	AX134866 Sequence
12	78	7.4	117	6	AX134963	AX134963 Sequence
13	78	7.4	117	6	AX135076	AX135076 Sequence
14	32	3.0	1373	9	HSROX40MR	X75962 H. sapiens m
15	28	2.6	618	6	AR019518	AR019518 Sequence
16	28	2.6	618	6	114933	114933 Sequence
17	28	2.6	883	10	MMOX40	221674 M. musculus
18	28	2.6	1317	6	AR019521	AR019521 Sequence
19	28	2.6	1317	6	114936	114936 Sequence
20	28	2.6	2907	10	MMDNAOX40	X85214 M. musculus
21	28	2.6	60953	2	AC100470	AC100470 Mus muscu
22	28	2.6	253111	2	AF627204	AF627204 Mus muscu
23	28	2.6	254197	2	AF389853	AF389853 Mus muscu
24	23	2.2	5148	6	AX251339	AX251339 Sequence
25	23	2.2	104480	2	AC007905	AC007905 Homo sapi
26	21	2.0	877	4	AB003911	AB003911 Rabbit mr
27	21	2.0	1420	9	BC002494	BC002494 Homo sapi
28	21	2.0	1569	6	AX202231	AX202231 Sequence
29	21	2.0	1632	9	HSR802071	AL137382 Homo sapi
30	21	2.0	1634	9	BC021574	BC021574 Homo sapi
31	21	2.0	4656	4	SSPROPLAU	X92447 S. scrofa pr
32	21	2.0	4657	4	SSY11872	Y11872 S. scrofa up
33	34	2.0	38640	1	SCL2	AL137778 Streptomy
34	21	2.0	120766	9	AC004150	AC004150 Homo sapi
35	21	2.0	139999	8	AC018727	AC018727 Oryza sat
36	21	2.0	175799	2	AC026583	AC026583 Homo sapi
37	21	2.0	184476	2	AC009113	AC009113 Homo sapi
38	21	2.0	185243	2	AC021958	AC021958 Homo sapi
39	21	2.0	189150	2	AL603804	AL603804 Mus muscu
40	21	2.0	200882	2	AL591181	AL591181 Homo sapi
41	21	2.0	202668	2	AC009715	AC009715 Homo sapi
42	21	2.0	214180	2	AL360082	AL360082 Homo sapi
43	21	2.0	218598	2	AC023855	AC023855 Homo sapi
44	21	2.0	300000	9	AL645813	AL645813 Human DNA
45	20	1.9	291	4	BOVBTB13	D90132 Bovine mRNA
46	20	1.9	1017	10	RSOX40	X17037 Rat mRNA fo
47	20	1.9	1995	10	MMU294749	AJ294749 Mus muscu
48	20	1.9	10309	1	AE003929	AE003929 Xylella f
49	20	1.9	12249	1	AE004632	AE004632 Pseudomon
50	20	1.9	26809	1	SC3A4	AL354616 Streptomy

ALIGNMENTS

RESULT	LOCUS	DEFINITION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	FEATURES	BASE COUNT
1	AR048669	Sequence 1 from patent US 5821332.	AR048669	GI:5971012	Unknown.	Unclassified.	1 (bases 1 to 1057)	Godfrey, W., Buck, D. and Engleman, E.G.	Receptor on the surface of activated CD4.sup.+ T-cells: ACT-4	Patent: US 5821332-A 1 13-OCT-1998;	Location/Qualifiers	176 a 390 c 344 g 147 t

601 ccagaaactcaaggaagaccctccaccgcccgttgaggctcccgaggcgctgctgctg 660
|||||
601 CCAGAACTCAAGGAGACCTCCACCCGGCGGTGAGGTCCCGGGCGCTGGGGTGG 660
Oy 661 ccgcacatctgggctgggctgctgctgctgctgctgctgctgctgctgctgctg 720
|||||
661 CCGCATCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 720
Db 721 ccccttactgtctgggaggagagagctgcccccgatgcccccaagagccccctgg 780
|||||
721 CCTTACTGCTGCTGGAGAGGACAGAGGCTGCCCGCATGCCACAGAGCCCTGGGG 780
Oy 781 gagagagttccggagaccaccatccaaagagagcagcagcagccacccacccctggcca 840
|||||
781 GAGGAGAGTTCCGGAGACCCCATCAAGAGAGACAGGCGAGCCGACCTCCAGCTGGCCA 840
Db 841 agatctgacatctgggcccacaaagtgagcgtctgggcccagagctggagccggagg 900
|||||
841 AGATCTGACC-TGGGCCCAACCAAGGTGAGACGCTGGGGCCCGCCAGAGCTGAGCCGAGG 899
Oy 901 gtctgtgaggagagagagagctgcaagcagcgtgccccgagcagcgtctctggccaact 960
|||||
901 GTCTGTGAGGAGAGGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 959
Db 961 ctgcacacgtctgaggctgcagatgctgctccgctctctgcttactgcttactgcatgcatgata 1020
|||||
960 CTGCACACGTTTCTAGGTGCGGATGGCTGCGGCTCTGCTTACGTATGCGCATGCGATATA 1019
Oy 1021 cctctgcccggcgaggaccacaataaaacttgagcag 1058
|||||
1021 CCTCTGCCCGCGGAGCCACAAATAAACCCTTGGCAG 1057
Db

RESULT 3
LOCUS S76792 1034 bp mRNA linear PRI 02-JUN-2000
DEFINITION OX40-cell surface antigen [human, mRNA Partial, 1034 nt].
ACCESSION S76792
VERSION S76792.1 GI:913405
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1034)
AUTHORS Baum,P.R., Gayle,R.B.III., Ramsdell,F., Srinivasan,S.,
Sorensen,R.A., Watson,M.L., Seldin,M.F., Clifford,K.N.,
Grabsstein,K., Alderson,M.R. et.al.
Identification of OX40 ligand and preliminary characterization of
its activities on OX40 receptor
Circ. Shock 44 (1), 30-34 (1994)
95219871
JOURNAL GenBank staff at the National Library of Medicine created this
MEDLINE entry [NCBI g1bbsq 163567] from the original Journal article.
REMARK This sequence comes from Fig. 3A.
FEATURES
source
1..1034
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene
<1..1034
/gene="OX40"
CDS
<1..825
/gene="OX40"
/note="cell surface antigen; This sequence comes from Fig.
3A"

1..1034
/organism="Homo sapiens"
/db_xref="taxon:9606"
gene
<1..1034
/gene="OX40"
CDS
<1..825
/gene="OX40"
/note="cell surface antigen; This sequence comes from Fig.
3A"

GLVLILPLAILALYLLRRDQRLPPAHKPPGGSFRTPEIOEQADAHSLAKI"
BASE COUNT 169 a 386 c 333 g 146 t
ORIGIN
Query Match 78.5%; Score 831; DB 9; Length 1034;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1001; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
Oy 26 ggtctggcgagctgggagcgagcgctgtgagctgtgctgtgctgtgagctgtgag 85
|||||
26 GGTCTGGCGAGCTGGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 62
Db 3 GGTCTGGCGAGCTGGGCGGCGGCGGCGGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 62
Oy 86 caacgtgagagggcttccactgtgtgtgagagacacttcccccaagagagcgtgtgtgcca 145
|||||
86 CACCGTAGAGGGGCTTCACCTGTGTGTGGAGACACTTACCCACAGACAGCGGTGCTGCA 122
Db 63 CACCGTAGAGGGGCTTCACCTGTGTGTGGAGACACTTACCCACAGACAGCGGTGCTGCA 122
Oy 146 cgagtgcagggcagagcaagagagatgtgagcagctgcaagcagctcccaagaacagtggtg 205
|||||
146 CGAGTGCAGGCGCAGGCAAGGAGATGTGAGCCGCTGACACCGCTCCACAGACAGGTTG 182
Db 123 CGAGTGCAGGCGCAGGCAAGGAGATGTGAGCCGCTGACACCGCTCCACAGACAGGTTG 182
Oy 206 ccgttcggtgggagcgagcttcttcaagagcgtgtgtcagctccaaagcgtgtcaagcctgt 265
|||||
206 CCGTCCGTGCGGCGGCGGCGGCTTACACAGACGCTGTGACCTCCAAAGCCTGCAAGCCCTG 242
Db 183 CCGTCCGTGCGGCGGCGGCGGCTTACACAGACGCTGTGACCTCCAAAGCCTGCAAGCCCTG 242
Oy 266 caggtgtgttaacctcaagaagtgtgagtgagcagagagcagctgtgtgacagcgccacacagga 325
|||||
266 CAGGTGTGTAACTTACCTCAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 302
Db 243 CAGGTGTGTAACTTACCTCAGAGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAGTGGAG 302
Oy 326 cacaagtctgcgctgcgagcgagcaccagccctgtgacagctacaagcctgtgaggttga 385
|||||
326 CACAAGTCTGCGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 362
Db 303 CACAGTCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 362
Oy 386 ctgtgcccccttccctccagggcacttctcccaagagcaacacagagcgtgtgaagccctgt 445
|||||
386 CTGTGCCCCCTTCCCTCCAGGGCAGCTTCTCCCAAGAGCAACACAGAGCAGAGCAGAGCAG 422
Db 363 CTGTGCCCCCTTCCCTCCAGGGCAGCTTCTCCCAAGAGCAACACAGAGCAGAGCAGAGCAG 422
Oy 446 gaccaaactgacacttggctgggagagacacacccctgtgacgagcgagcaagatagctgcagc 505
|||||
446 GACCAACTGACACTTGGCTGGGAGAGACACACCCCTGTGACGAGCGAGCAAGATAGCTGCAG 482
Db 423 GACCAACTGACACTTGGCTGGGAGAGACACACCCCTGTGACGAGCGAGCAAGATAGCTGCAG 482
Oy 506 aatctgtgagagagagagaccccccagcagcagcagcagcagcagcagcagcagcagcagcagc 565
|||||
506 AATCTGTGAGGAG 542
Db 483 AATCTGTGAGGAG 542
Oy 566 cagggccatcatctgttcaagacccacttgaagcctgtgagcccaagactcaagagagcctccac 625
|||||
566 CAGGCCATCATCTGTTCAGACCCCACTGAAGCCTTGAGCCCAAGACTCAAGAGAGCCTCCAC 602
Db 543 CAGGCCATCATCTGTTCAGACCCCACTGAAGCCTTGAGCCCAAGACTCAAGAGAGCCTCCAC 602
Oy 626 ccggcccgctggagaggtcccgaggagccgtgtgagcttgcagcatccctggcctggagcctgtgt 685
|||||
626 CCGGCCCGCTGGAGAGGTCCCGGGGGCGGTGCGGTGCGGCATCTGCGGCTGGGCTGGGT 662
Db 603 CCGGCCCGCTGGAGAGGTCCCGGGGGCGGTGCGGTGCGGCATCTGCGGCTGGGCTGGGT 662
Oy 686 gcttgagagctgtgagcctccctgtgcaactctgtgctgtgacactgtgtcctgagagagca 745
|||||
686 GCTTGAGAGCTGTGAGCCCTCCCTGTGCAACTCTGTGCTGTGACCTGTGCTGCTGCTGCTG 722
Db 663 GCTTGAGAGCTGTGAGCCCTCCCTGTGCAACTCTGTGCTGTGACCTGTGCTGCTGCTGCTG 722
Oy 746 gaggctgcccccgatagcccaagagccctgtggagagagcttccggaaccccatcca 805
|||||
746 GAGGCTGCCCGGATAGCCCAAGAGCCCTGTGGAGAGAGCTTCCGGAACCCCATCCA 805
Db 723 GAGGCTGCCCGGATAGCCCAAGAGCCCTGTGGAGAGAGCTTCCGGAACCCCATCCA 805
Oy 806 agagagagagcagagcagccacttcaacccctgtgcaagatctgaacttgggccaacaag 865
|||||
806 AAGAGAGAGAGCGAGCGGAGAGCCCACTCCAGCTGCGCAAGATCTGACC-TGGGCCACAGAG 841
Db 783 AAGAGAGAGAGCGGAGAGCCCACTCCAGCTGCGCAAGATCTGACC-TGGGCCACAGAG 841
Oy 866 tggagcgtgtggcccgagcagctgtgagcccgagaggtctgtctgtggcgagcagagcagtg 925
|||||
866 TGGAGCGTGTGGCCCGAGCGAGCTGTGAGCCCGAGAGGTCTGTCTGTGGGAGCAGGCGAGGTG 901
Db 842 TGGAGCGTGTGGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 901
Oy 926 cagggccgcttgcgagcagcagcgtctcctgggagcaacttgcagcgtttcaggtgcagatgc 985
|||||
926 CAGGCCCGCTGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 961
Db 902 CAGGCCCGCTGCCCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 961

QY	986	1gcctccgagctctcgtctacgtatgcacatgaatccctctgc	1028
Db	962	tgccctccgagctctcgtctacgtatgcacatgaatccctctgc	1004
RESULT	4		
LOCUS	HSBOX40MR	1373 bp	Linear
DEFINITION	H.sapiens mRNA for OX40 homologue.		
ACCESSION	X75962		
VERSION	X75962.1	GI:472957	
KEYWORDS	OX40 antigen.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Latza, U., Dufkop, H., Schnitger, S., Ringeling, J., Eitelbach, F., Hummel, M., Parnisch, C. and Stein, H.		
TITLE	The human OX40 homology: cDNA structure, expression and chromosomal assignment of the ACR35 antigen		
JOURNAL	Eur. J. Immunol. 24 (3), 677-683 (1994)		
MEDLINE	94170844		
REFERENCE	2 (bases 1 to 1373)		
AUTHORS	Latza, U.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz, Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG		
FEATURES	source		
	1..1373		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
CDS	6..839		
	/codon_start=1		
	/product="OX40 homologue"		
	/protein_id="CAA53576.1"		
	/db_xref="GI:472958"		
	/db_xref="SWISS-PROT:P43489"		
	/translation="MCVGARRLRGRCPCALLLLGLSTVTGLHCVDPTYSNDRCHECRGNNGNSRCSRSNTVCPCPGFINDVSSKPCPCWNCNLRSSERKOLCTAIAQDVCRCRAGTQPLDSTKPGVDCAPCPGPHSPGDNDACKPMWNTCTLAGKHTLQPASLSDICEDRPDPAPQDETGPAPRPATVVOPTFEMPRTSGSPRPVPEVPGRAVVAALGLTGLVGLGLPLAILALYLRLRDORLPRPAHKRPGGGSRFRLPDEQADAHSTLAKM I"		
	1..89		
	sig_peptide		
	90..836		
	mat_peptide		
	814..958		
	repeat_region		
	959..1079		
	polya_signal		
	1341..1346		
	polya_site		
	1358		
BASE COUNT	257 a 452 c 423 g 241 t		
ORIGIN			
	Query Match	69.9%	Score 740; DB 9; Length 1373;
	Best Local Similarity	99.8%;	Pred. No. 0;
	Matches 840; Conservative	0; Mismatches	2; Indels 0; Gaps 0;
QY	10	cgagagatgtcgttgggggtcggagcgtcggagccggagccggtgtgagcgtctgtctctcc	69
Db	1	CGAGATGTGCTGGGGGCTCGCGCGCTGGGGCGCGGCGCGGTCTGCTCTTC	60
QY	70	tggagctggggctcgagacacgtgaaggggcttcacatgtgtcggaggacacatccccaaga	129
Db	61	TGGGCTGGGGCTGAGACACGAGAGGGGCTTCACATGTGTGCGGGACACATCCACAGA	120
QY	130	acgacacggtgtctgcacagatgcaggtcaggtcgaacaggatggtgagccgctgcagcgct	189
Db	121	ACGACCGGTGTCTGCACAGATGCACAGCCACAGGCAACGGGATGGTGAAGCCGTCACGCGT	180
QY	190	ccaggaacaggtgtgagcgttcggtgtgaggtccggggtcttcaacagacgtgtcagctcca	249

D	b	181	CCGACAAACAGCGTGTGGCGTGCTCCGTGCCGTGCAGGCGCGGCTTTCTACACAGACAGTGGTCACACTCCA	240
O	y	250	agccgttgaagaagccttcgcgltggttgtaacctagaagtggaggatgaagcaagcagttgt	309
D	b	241	AGCCCTGCAAGCCTTGACAGTGTGTAAACCTCAGAATGTGGAGTAGCAGCGAAGCAGCTGT	300
O	y	310	gccagcgccaacacaaggaaacaagtctgcgcgtctgcggagcgaggcaaccagccccttgacaagt	369
D	b	301	GCACGGCCACACAGGACACAGTCTCCGCTGCCGGCGGGCACCCACAGCCCCCTGGACAGCT	360
O	y	370	aaaagccgggaattgaactcgtgccccctgcgcctccacagggaactctctcccaaggcgaacaac	429
D	b	361	ACAACCCTGGAGATTACTGTGTGCCCTTCGCTCCACAGGCGACTTCTTCCCAGCGACAAAC	420
O	y	430	aggccttgaagcccttgaagccaacttgcaccttgccttggcttggaaagacacaccccttgcagccgca	489
D	b	421	AGGCTTGCAAGCCCTYGACAACTGCACCTTGGCTTGGGAAGCACACCTGCAAGCCGGCCA	480
O	y	490	gcaataagcttggagcgaatctgttggagaaagggaacccccagccgacgcaagcccaaggaga	549
D	b	481	GCAATAAGCTCGGACCAATCTGTGTAGGACAGGAGACCCCCACACGACGACCCCAAGAAA	540
O	y	550	cccaaaggccccccggcgccagagcccatcatctgtccaaagcccaacttgaagcccgagcaaacct	609
D	b	541	CCCAAGGCCCCCGGCGCAGGCCCATCTGTCTGACGCCACTTAAGCTTGCCGCAAACTT	600
O	y	610	cacaaggaaacctcacaaccggccgcttgaaggttccccggggcggttgcgttgcgcgcatcc	669
D	b	601	CACAGGAGCCCTTCCACCCGCGCGGTGGAGATGCCCGGGGGCGGTGCGGTGCCGCAATTC	660
O	y	670	tggagccttggagccttgttgggtgctgcgtcgggagcccccttggcatactctgtgccccgtacc	729
D	b	661	TGGGCTTGTGGCTGTGTGCTGGGGCTGTGTGGCCCCCTTGCCCAATCTGTGTGCGCTGTAC	720
O	y	730	tgcctcgaaggaggaaccaaggagctgtccccccgatatgccaaagagcccccttggggaggaagcatt	789
D	b	721	TGCTTCGGAGGAGGACACAGAGCTGCGCCCCCGATGCCCAAAAGCCCTTGGGGAGGCACTT	780
O	y	790	tccggaaccccccatccaaaggagacagagccgacgcgcccacttcaaccttggccaagatctgac	849
D	b	781	TCCGGAACCCCATCCMAAGAGGAGCGCGGAGGCCCACTCCACCTTGCGCAAAGATCTGAC	840
O	y	850	ct 851	
D	b	841	CT 842	
<hr/>				
R	E	S		
L	O	C	HSA277151	5150 bp DNA linear PRI 05-JUL-2000
D	E	F	HSN277151	
I	N	F	Homo sapiens ox40 gene for CD134 antigen, exons 1-7.	
A	C	C	AJ277151	
V	E	R	AJ277151.1 GI:8926701	
K	E	Y	CD134 antigen; OX40 gene; rat OX40 antigen homologue.	
W	A	S	human.	
O	R	G	Homo sapiens	
R	E	F	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
A	U	T	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
R	E	F	1 (bases 1 to 5150)	
A	U	T	Latza,U., Durkop,H., Schnittiger,S., Ringeling,J., Etelbach,F.,	
T	I	T	Hummel,M., Fonatsch,C. and Stein,H.	
T	I	T	The human OX40 homology: cDNA structure, expression and chromosomal	
J	O	R	assignment of the ACT35 antigen	
R	E	F	Eur. J. Immunol. 24 (3), 677-683 (1994)	
A	U	T	9410844	
J	O	R	2 (bases 1 to 5150)	
R	E	F	Pankov,R., Durkop,H., Latza,U., Krause,H., Kunzendorf,U., Pohl,T.	
A	U	T	and Bulfone-Paus,S.	
T	I	T	The HIV-1 tax protein transcriptionally modulates OX40 antigen	
J	O	R	expression	
R	E	F	J. Immunol. 165 (1), 263-270 (2000)	
A	U	T	20318724	
R	E	F	3 (bases 1 to 5150)	

FEATURES	COMMENT
JOURNAL TITLE	Pankow, R.
Direct Submission	Submitted (28-MAR-2000) Pankow R., Inst. of Immunology, FU Berlin, University Hospital Benjamin Franklin, Hindenburgdamm 30, 12200 Berlin, GERMANY
Related sequence X75962.	location/qualifiers
source	1..5150
organism	"Homo sapiens"
taxon	"9606"
join	(1267..1437,1635..1757,2328..2429,2717..2783,
3284..3480,3590..3718,3797..4096)	
gene	/gene="Ox40"
1267..4096	
gene	"Ox40"
1267..1292	
gene	"Ox40"
1267..1437	
gene	"Ox40"
number=1	
join	(1293..1437,1635..1757,2328..2429,2717..2783,
3284..3480,3590..3718,3797..3867)	
gene	"Ox40"
note	"rat Ox40 antigen homologue"
codon_start=1	
product	"CD134 antigen"
protein_id	"CAB96543.1"
db_xref	"GI:8926702"
translation	"MVGARLRGRPCALLLLGLGISTVTGLHCVDGYPSNDRCH ECRCRGMVSRCSRSOMVPCPGPGYNDVSSPKPCMCYLREGSEPKCTMT ODYCRKRAQTPLDSYKPGVDCAPCPGPHSPEDNDACKRWTCITLAKHTLPASN SSDIDCEDRDPPATQPEOTGPPARPITVOPTEMPRTSQGPSTRPVEPVGGRNAVAI IGLGLVLGLEPLAILALYLRLRRDRLPPDAHKPPGGSFRPIOEADAHSTLARK I"
intron	1438..1634
gene	"Ox40"
number=1	
1635..1757	
gene	"Ox40"
number=2	
1758..2327	
gene	"Ox40"
number=2	
2328..2429	
gene	"Ox40"
number=3	
2430..2716	
gene	"Ox40"
number=3	
2717..2783	
gene	"Ox40"
number=4	
2784..3283	
gene	"Ox40"
number=4	
3284..3480	
gene	"Ox40"
number=5	
3481..3589	
gene	"Ox40"
number=5	
3590..3718	
gene	"Ox40"
number=6	
3719..3796	
gene	"Ox40"
number=6	
3797..4096	
gene	"Ox40"
number=7	
3868..4096	
gene	"Ox40"
3930..4096	

Query Match	Best Local Similarity	100.0%;	Pred. No. 2.9e-93;	Matches 207;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 852	tgggcccaacaaagtgtgaagctgtggcccgccagagctgtgagccggaaggtctgtgagc 911							
Db 3870	TGGGCCCAACAAGGTGAGACGTGGGCCGCCGCCAGGCTGGAGCCGAGGCTGCTGGGGC 3929							
QY 912	gagcagggcgaagtgtgaagccgcgtccgcgcgaagctctctgggccaactctgacagcttc 971							
Db 3930	GAGCAGGGCAGGTGAGAGGCCCTCTCCGCCACACCTCTGTGGCCCACTGTGACCCGTTTC 3989							
QY 972	taggtgcagatgtgcgtccctgcggtctctgtcttaagatgtgcataaccctctgcccc 1031							
Db 3990	TAGGTGCCGATGGTGCCTCCGGCTCTGCTGTACTGATGCAATGCATACCTCTCGCCCC 4049							
QY 1032	gcggagccacaataaaccttggcag 1058							
Db 4050	GCGGAGCACCAATTAACCTTGGCAG 4076							
RESULT 6	AL162741	111119 bp	DNA	linear	HTG 08-FEB-2002Z			
LOCUS	AL162741							
DEFINITION	Homo sapiens chromosome 1 clone RP5-902P8, *** SEQUENCING IN							
ACCESSION	AL162741							
VERSION	AL162741.24	GI:18643745						
KEYWORDS	HTGS; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.							
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
TITLE	1 (sites)							
JOURNAL	Harrison,E.							
COMMENT	Direct Submission							
	Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,							
	Cambridgeshire, CB10 1SA, UK. E-mail enquiries:							
	humquerry@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk							
	On Feb 10, 2002 this sequence version replaced gi:18642353.							
	----- Genome Center							
	Center: Wellcome Trust Sanger Institute							
	Center code: SC							
	Web site: http://www.sanger.ac.uk							
	Contact: humquerry@sanger.ac.uk							
	----- Project Information							
	Center project name: dj902P8							

```

----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 16% of reads Chemistry:
Dye-terminator Big Dye; 83% of reads
Consensus quality: 110490 bases at least Q40
Consensus quality: 110677 bases at least Q30
Consensus quality: 110755 bases at least Q30
Insert size: 110819; sum-of-contigs
Insert size: 160089; 6.7% error; agarose-fp
Quality coverage: 8.36x in Q20 bases; sum-of-contigs quality
coverage: 5.95x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 42985: contig of 42985 bp in length
* 42986 43085: gap of 100 bp
* 43086 54937: contig of 11852 bp in length
* 54938 55037: gap of 100 bp
* 55038 67254: contig of 12217 bp in length
* 67255 67354: gap of 100 bp
* 67355 111119: contig of 43765 bp in length.
Location/Qualifiers
1. 111119
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP5-902P8"
/clone_lib="RPC1-5"
1. 42985
/note="assembly-fragment:00240
fragment_chain:1
clone_end:SP6
vector_side:left"
43086. 54937
/note="assembly-fragment:02853
fragment_chain:1"
55038. 67254
/note="assembly-fragment:00075
fragment_chain:1"
67355. 111119
/note="assembly-fragment:02810
fragment_chain:1"

misc_feature
BASE COUNT 22049 a 35882 c 32333 g 20555 t 300 others
ORIGIN

Query Match 19.6%; Score 207; DB 2; Length 111119;
Best Local Similarity 100.0%; Pred. No. 1.9e-93;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 852 tggggccaccacgaagtgagcgtggcccgccagcgtgagccggagggctgctgggc 911
|||||
DB 21664 TGGGCCACCAAGGTGAGCTGGCCCGCCAGCGCTGAGCCCGAGCGCTGTGCGGC 21605
|||||
QY 912 gagcaggcaggtgacgagcgcctgcccgcacgctcctgggccaactctgacgcttc 971
|||||
DB 21604 GACCAAGGCGGTGAGCGCGCTGCCCGCCAGCTCTCGGGCCAACTCTGACCGTTC 21545
|||||
QY 972 taagtgccgatggctgctcccgctcttgcttaagctatgcatgcatgctgcccc 1031
|||||
DB 21544 TAGGTCGCATGGCTGCTCGGCTCTGTGCTTACGTATGCCATGCTGCTGCCCC 21485
|||||
QY 1032 gcggagccacataaaaccttggcag 1058
|||||
DB 21484 GCGGAGCACCAATAAACCTTGCGAG 21458
|||||

```

```

RESULT 7
AL390719
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Homo sapiens chromosome 1 clone RP11-465B22, *** SEQUENCING IN
PROGRESS ***, 29 unordered pieces.
AL390719.25 GI:18476612
HTG: HTGS_PHASE1; HTGS_DRAFT.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (sites)
McLay, K.
Direct Submission
Submitted (24-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:16304463.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BA465B22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 2% of reads Chemistry:
Dye-terminator Big Dye; 97% of reads
Consensus quality: 201072 bases at least Q40
Consensus quality: 204266 bases at least Q30
Consensus quality: 206043 bases at least Q20
Insert size: 208144; sum-of-contigs
Insert size: 227650; 6.6% error; agarose-fp
Quality coverage: 5.63x in Q20 bases; sum-of-contigs quality
coverage: 5.53x in Q20 bases; agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 8088: contig of 8088 bp in length
* 8089 8168: gap of 100 bp
* 8169 23213: contig of 15025 bp in length
* 23214 23313: gap of 100 bp
* 23314 27220: contig of 3907 bp in length
* 27221 27320: gap of 100 bp
* 27321 30326: contig of 3006 bp in length
* 30327 30426: gap of 100 bp
* 30427 43166: contig of 12740 bp in length
* 43167 43266: gap of 100 bp
* 43267 47516: contig of 4250 bp in length
* 47517 47616: gap of 100 bp
* 47617 51392: contig of 3776 bp in length
* 51393 51492: gap of 100 bp
* 51493 60771: contig of 9279 bp in length
* 60772 60871: gap of 100 bp
* 60872 63164: contig of 2293 bp in length
* 63165 63264: gap of 100 bp
* 63265 69307: contig of 6043 bp in length
* 69308 69407: gap of 100 bp
* 69408 76647: contig of 7240 bp in length
* 76648 76747: gap of 100 bp
* 76748 98297: contig of 21550 bp in length
* 98298 98397: gap of 100 bp
* 98398 100781: contig of 2384 bp in length

```

```
* 100782 100881: gap of 100 bp
* 100882 108287: contig of 7406 bp in length
* 108288 108387: gap of 100 bp
* 108388 116410: contig of 8023 bp in length
* 116411 116510: gap of 100 bp
* 116511 119166: contig of 2656 bp in length
* 119167 119266: gap of 100 bp
* 119267 121683: contig of 2417 bp in length
* 121684 121783: gap of 100 bp
* 121784 125415: contig of 3632 bp in length
* 125416 125515: gap of 100 bp
* 125516 132751: contig of 7236 bp in length
* 132752 132851: gap of 100 bp
* 132852 137874: contig of 5023 bp in length
* 137875 137974: gap of 100 bp
* 137975 147639: contig of 9665 bp in length
* 147640 147739: gap of 100 bp
* 147740 150747: contig of 3008 bp in length
* 150748 150847: gap of 100 bp
* 150848 154411: contig of 3564 bp in length
* 154412 154511: gap of 100 bp
* 154512 180672: contig of 26161 bp in length
* 180673 180772: gap of 100 bp
* 180773 187118: contig of 6346 bp in length
* 187119 187218: gap of 100 bp
* 187219 197762: contig of 10544 bp in length
* 197763 197862: gap of 100 bp
* 197863 203431: contig of 5569 bp in length
* 203432 203531: gap of 100 bp
* 203532 206862: contig of 3331 bp in length
* 206863 206962: gap of 100 bp
* 206963 210944: contig of 3962 bp in length.
Location/Qualifiers
1. 210944
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
/clone="RP11-465B22"
/clone_lib="RPC1-11.2"
1. 8088
/note="assembly_fragment:00856
fragment_chain:1
clone_end:77
vector_side:left"
8189. 23213
/note="assembly_fragment:02699
fragment_chain:1"
23314. 27220
/note="assembly_fragment:02428
fragment_chain:1"
27321. 30326
/note="assembly_fragment:02062
fragment_chain:1"
30427. 43166
/note="assembly_fragment:00183
fragment_chain:2"
43267. 47516
/note="assembly_fragment:02637
fragment_chain:2"
47617. 51392
/note="assembly_fragment:00819
fragment_chain:2"
51493. 60771
/note="assembly_fragment:03852
fragment_chain:2"
60872. 63164
/note="assembly_fragment:02567
fragment_chain:2"
63265. 69307
/note="assembly_fragment:04648
fragment_chain:2"
69408. 76647
/note="assembly_fragment:00506
```

```
misc_feature      fragment_chain:2"
76748. 98297
/note="assembly_fragment:05288
fragment_chain:2"
98398. 100781
/note="assembly_fragment:00325
fragment_chain:3"
100882. 108287
/note="assembly_fragment:03939
fragment_chain:3"
108388. 116410
/note="assembly_fragment:01362
fragment_chain:3"
116511. 119166
/note="assembly_fragment:05470
fragment_chain:3"
119267. 121683
/note="assembly_fragment:00386
fragment_chain:4"
121784. 125415
/note="assembly_fragment:03427
fragment_chain:4"
125516. 132751
/note="assembly_fragment:00351
fragment_chain:4"
132852. 137874
/note="assembly_fragment:01398
fragment_chain:4"
137975. 147639
/note="assembly_fragment:03656
fragment_chain:5"
147740. 150747
/note="assembly_fragment:05495
fragment_chain:5"
150848. 154411
/note="assembly_fragment:00729
fragment_chain:5"
154512. 180672
/note="assembly_fragment:01493
fragment_chain:5"
180773. 187118
/note="assembly_fragment:00254
fragment_chain:6"
187219. 197762
/note="assembly_fragment:04216
fragment_chain:6"
197863. 203431
/note="assembly_fragment:00160"
203532. 206862
/note="assembly_fragment:03327"
206963. 210944
/note="assembly_fragment:04407"
BASE COUNT      38968 a 62852 c 66926 g 39385 t 2813 others
ORIGIN
```

Query Match 19.6%; Score 207; DB 2; Length 210944;
Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 852 tgggccaccaaggtgagcgtggccgcgacgagctgagagccgcgagggctgctggc 911
|||||
DB 9182 TGGGCCACCAAGGTGAGCTGGCCGCCGCGACGCTGAGCCCGGAGGGCTGCTGGGC 9241
QY 912 gaccaaggcaggtgcaagcgccctggccgcgacgagctccgggccaactctgcaacgctt 971
|||||
DB 9242 GAGCAGGGCAGGTGACGAGCGCCCTGCCCCGACGCTCTGGGCCAAGCTTGACCGCTTC 9301
QY 972 taagtgcgatagtgctgcctccgagctctctgcttaagatgacatgcatgcatctctggccc 1031
|||||
DB 9202 TAGTGCCGAGAGGCTGCTCCGGCTCTCTGCTTACGATGCAATGCAATACCTCTGCCCC 9361
QY 1032 gcgggaccacaataaaaccttgag 1058
```

Db 9362 GCGGACACAAATAAAACCTTGCAg 9388
|||||
RESULT 8
AX134865 117 bp DNA linear PAT 29-MAY-2001
LOCUS Sequence 58 from Patent WO0132709.
DEFINITION AX134865
ACCESSION AX134865.1 GI:14271353
VERSION
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 117)
AUTHORS Finney,H.M. and Lawson,A.D.
TITLE Polypeptides with non-natural primary signalling motifs
JOURNAL Patent: WO 0132709-A 58 10-MAY-2001;
Celltech Chiroscience Limited (GB)
FEATURES
source 1. 117
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide for chimeric receptor construction"
BASE COUNT 25 a 45 c 36 g 11 t
ORIGIN
Query Match 7.8%; Score 83; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-30;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 735 cggagggaccagaggtgcggcccgatgcccacaaagcccccctggggagagcagttccgg 794
|||||
Db 6 CCGAGGACCAAGAGGCTGCCGCCGATGCCACAAAGCCCCCTGGGAGGACAGTTCCGG 65
Qy 795 acccccatccaagagagcagc 817
|||||
Db 66 ACCCCATCCAAAGAGGACGAGC 88
RESULT 9
AX134962 117 bp DNA linear PAT 29-MAY-2001
LOCUS AX134962
DEFINITION Sequence 73 from Patent WO0132867.
ACCESSION AX134962
VERSION AX134962.1 GI:14271404
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 117)
AUTHORS Finney,H.M. and Lawson,A.D.
TITLE Polypeptides with expanded primary signalling motifs
JOURNAL Patent: WO 0132867-A 73 10-MAY-2001;
Celltech Chiroscience Limited (GB)
FEATURES
source 1. 117
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Chimeric receptor construction oligonucleotide
F1340A"
BASE COUNT 25 a 45 c 36 g 11 t
ORIGIN
Query Match 7.8%; Score 83; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-30;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 735 cggagggaccagaggtgcggcccgatgcccacaaagcccccctggggagagcagttccgg 794
|||||
Db 6 CCGAGGACCAAGAGGCTGCCGCCGATGCCACAAAGCCCCCTGGGAGGACAGTTCCGG 65

Qy 795 acccccatccaagagagcagc 817
|||||
Db 66 ACCCCATCCAAAGAGGACGAGC 88
RESULT 10
AX135075 117 bp DNA linear PAT 29-MAY-2001
LOCUS AX135075
DEFINITION Sequence 88 from Patent WO0132866.
ACCESSION AX135075
VERSION AX135075.1 GI:14271470
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 117)
AUTHORS Finney,H.M. and Lawson,A.D.
TITLE Hybrid adaptor receptors
JOURNAL Patent: WO 0132866-A 88 10-MAY-2001;
Celltech Chiroscience Limited (GB)
FEATURES
source 1. 117
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Adaptor receptor construction oligonucleotide
F1340A"
BASE COUNT 25 a 45 c 36 g 11 t
ORIGIN
Query Match 7.8%; Score 83; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 1.7e-30;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 735 cggagggaccagaggtgcggcccgatgcccacaaagcccccctggggagagcagttccgg 794
|||||
Db 6 CCGAGGACCAAGAGGCTGCCGCCGATGCCACAAAGCCCCCTGGGAGGACAGTTCCGG 65
Qy 795 acccccatccaagagagcagc 817
|||||
Db 66 ACCCCATCCAAAGAGGACGAGC 88
RESULT 11
AX134866/C 117 bp DNA linear PAT 29-MAY-2001
LOCUS AX134866/C
DEFINITION Sequence 59 from Patent WO0132709.
ACCESSION AX134866
VERSION AX134866.1 GI:14271354
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 117)
AUTHORS Finney,H.M. and Lawson,A.D.
TITLE Polypeptides with non-natural primary signalling motifs
JOURNAL Patent: WO 0132709-A 59 10-MAY-2001;
Celltech Chiroscience Limited (GB)
FEATURES
source 1. 117
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Oligonucleotide for chimeric receptor construction"
BASE COUNT 11 a 35 c 45 g 26 t
ORIGIN
Query Match 7.4%; Score 78; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.8e-28;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 768 aagccccctggggagagcagttccggaccaccatccaagagagcagcagccac 827

Db 83 AGCCCCCTGGGGGAGGAGCGAGTTCCGACCCCATCCAGAGAGAGCGCGCAGCCGCAC 24
QY 828 tccacctgagccaagatc 845
Db 23 TCCACCCTGGCCAGATC 6

RESULT 12
AX134963/c 117 bp DNA linear PAT 29-MAY-2001

LOCUS AX134963
DEFINITION Sequence 74 from Patent W00132867.
ACCESSION AX134963
VERSION AX134963.1 GI:14271405

KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 117)
AUTHORS Finney,H.M. and Lawson,A.D.

TITLE Polyptides with expanded primary signalling motifs
JOURNAL Patent: WO 0132867-A 74 10-MAY-2001;
Celltech Chiroscience Limited (GB)

FEATURES
Location/Qualifiers
1..117

BASE COUNT 11 a 35 c 45 g 26 t
ORIGIN
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Chimeric receptor construction oligonucleotide
F1340B"

Query Match 7.4%; Score 78; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.8e-28;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 768 aagcccccctggggagagcgagttccggaccccatccaagagagcgagcgccac 827
Db 83 AAGCCCCCTGGGGGAGGAGCGAGTTCCGACCCCATCCAGAGAGAGCGCGCAGCCGCAC 24

QY 828 tccacctgagccaagatc 845
Db 23 TCCACCCTGGCCAGATC 6

RESULT 13
AX135076/c

LOCUS AX135076 117 bp DNA linear PAT 29-MAY-2001
DEFINITION Sequence 89 from Patent W00132866.
ACCESSION AX135076
VERSION AX135076.1 GI:14271471

KEYWORDS
SOURCE synthetic construct.
ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 117)
AUTHORS Finney,H.M. and Lawson,A.D.

TITLE Hybrid adaptor receptors
JOURNAL Patent: WO 0132866-A 89 10-MAY-2001;
Celltech Chiroscience Limited (GB)

FEATURES
Location/Qualifiers
1..117

BASE COUNT 11 a 35 c 45 g 26 t
ORIGIN
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Adaptor receptor construction oligonucleotide
F1340B"

Query Match 7.4%; Score 78; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.8e-28;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 768 aagcccccctggggagagcgagttccggaccccatccaagagagcgagcgccac 827

Db 83 AAGCCCCCTGGGGGAGGAGCGAGTTCCGACCCCATCCAGAGAGAGCGCGCAGCCGCAC 24

QY 828 tccacctgagccaagatc 845
Db 23 TCCACCCTGGCCAGATC 6

RESULT 14
HSHOX40MR/c 1373 bp mRNA linear PRI 13-MAY-1994

LOCUS HSHOX40MR
DEFINITION H.sapiens mRNA for OX40 homologue.
ACCESSION X75962
VERSION X75962.1 GI:472957

KEYWORDS OX40 antigen.
SOURCE human.
ORGANISM human sapiens

REFERENCE 1 (bases 1 to 1373)
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
Hummel,M., Fonatsch,C. and Stein,H.

TITLE The human OX40 homologue: cDNA structure, expression and chromosomal
assignment of the AC35 antigen

JOURNAL Eur. J. Immunol. 24 (3), 677-683 (1994)
MEDLINE 94170844
REFERENCE 2 (bases 1 to 1373)

AUTHORS Latza,U.
JOURNAL Direct Submission
TITLE Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz,
Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG

FEATURES
Location/Qualifiers
1..1373

CDs
/organism="Homo sapiens"
/db_xref="taxon:9606"
6..839
/codon_start=1
/product="OX40 homologue"
/protein_id="CA53576.1"

/db_xref="GI:472958"
/db_xref="SWISS-PROT:P43489"
/translation="MCVGARRLRGRCALILGLSTVTGLHCVDTPSNDRCCH
BCRPGNWSRCSRSQNTVCRPGFNDVYSSRCKPCNTCRSGSERLOCTAT
ODTVRCRAGQPLDYSKRGVDCACRPGHSGPQNOACKPTNTLAKHILQASN
SSDATICRBDPPATPOTQCPARPPTVOTPEANPRISQGSTPVEYGGRAVAAI
LGGLVIGLGLPLALILALYLLRQRLPPDAHRRPQGSGSFPTIOERQADAHSTLAK
I"

sig_peptide 6..89
mat_peptide 90..836
/product="OX40 homologue"

repeat_region 814..958
repeat_region 959..1079
polya_signal 1341..1346
polya_site 1358

BASE COUNT 257 a 452 c 423 g 241 t
ORIGIN

Query Match 3.0%; Score 32; DB 9; Length 1373;
Best Local Similarity 100.0%; Pred. No. 6.6e-05;

Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 852 tgggcccaccagtggaagctgagcccgcc 883
Db 930 TGGGCCACCAAGTGAGCGTGGCCCGCC 899

RESULT 15
AR019518 618 bp DNA linear PAT 05-DEC-1998

LOCUS AR019518

Query Match 7.4%; Score 78; DB 6; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.8e-28;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

DEFINITION Sequence 6 from patent US 5783665.
ACCESSION AR019518
VERSION AR019518.1 GI:3974632
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 618)
AUTHORS
  Baum, P. R., Fanslow, W. C. III, Gayle, R. B. and Goodwin, R. G.
TITLE
  Cytokine which is a ligand for OX40
JOURNAL
  Patent: US 5783665-A 6 21-JUL-1998;
FEATURES
  source
    1.618
    /organism="unknown"
BASE COUNT      148 a      187 c      151 g      132 t
ORIGIN

Query Match      2.6%; Score 28; DB 6; Length 618;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 acaccagcctgcaagcctggaccac 451
Db 404 ACAACGAGCCTGCAAGCCTGGACCAA 431

RESULT 16
LOCUS      114933      618 bp      DNA      linear      PAT 02-APR-1996
DEFINITION Sequence 6 from patent US 5457035.
ACCESSION      114933
VERSION      114933.1 GI:1249842
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 618)
AUTHORS
  Baum, P. R., Fanslow, W. C. III, Gayle, R. B. and Goodwin, R. G.
TITLE
  Cytokine which is a ligand for OX40
JOURNAL
  Patent: US 5457035-A 6 10-OCT-1995;
FEATURES
  source
    1.618
    /organism="unknown"
BASE COUNT      148 a      187 c      151 g      132 t
ORIGIN

Query Match      2.6%; Score 28; DB 6; Length 618;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 acaccagcctgcaagcctggaccac 451
Db 404 ACAACGAGCCTGCAAGCCTGGACCAA 431

RESULT 17
LOCUS      MMOX40      883 bp      mRNA      linear      ROD 20-DEC-1993
DEFINITION M.musculus OX40.
ACCESSION      221674
VERSION      221674.1 GI:312827
KEYWORDS
  OX40.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 883)
AUTHORS
  Calderhead, D. M., Buhmann, J. E., van den Eertwegh, A. J., Claassen, E.,
  Noelle, R. J. and Felli, H. P.
TITLE
  Cloning of mouse OX40: a T cell activation marker that may mediate
  T-B cell interactions

```

```

JOURNAL      J. Immunol. 151 (10), 5261-5271 (1993)
MEDLINE      94044750
REFERENCE      2 (bases 1 to 883)
AUTHORS
  Calderhead, D. M.
TITLE
  Direct Submission
JOURNAL
  Submitted (11-FEB-1993) David M Calderhead, Molecular Immunology,
  Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First
  Ave., Seattle, WA, 98121, USA
FEATURES
  source
    1.883
    /organism="Mus musculus"
    /strain="Balb/c"
    /db_xref="taxon:10090"
    /clone="pUCox40.RJ.1"
    /cell_line="TH2 D.10"
    /cell_type="T-helper cell1"
    1.819
    /codon_start=1
    /product="OX40"
    /protein_id="CAA79772.1"
    /db_xref="GI:312828"
    /db_xref="MGI:104512"
    /db_xref="MGI:MGI:104512"
    /translation="MYVWVOOPFALLALITLGYTARINCYKHYTPSGHKCCRECP
    GHGWSRCDHTPTDILCHPCETCFYNNAVNYDCKOCOTOCNHRSGSLKNCPTPDIV
    CRRPETOPIRDSGKILGYDVPCEPGHSPGNQACKPWICTLSGKOTRIPASDL
    DAVCEDRSLLATLWETORPRTPTVOSTVWPRISLSPPTLVTPGPAFVILG
    LGLGLAPLTVLALYLILKAWRLPTPKPCWGNSPRPIDOEHDHPTLAKI"
    1.57
    /note="rat specific PCR primer"
    1.21
    /note="rat specific PCR primer"
    58.816
    /product="OX40"
    860.883
    /note="rat specific PCR primer"
BASE COUNT      201 a      269 c      220 g      193 t
ORIGIN

Query Match      2.6%; Score 28; DB 10; Length 883;
Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 acaccagcctgcaagcctggaccac 451
Db 404 ACAACGAGCCTGCAAGCCTGGACCAA 431

RESULT 18
LOCUS      AR019521      1317 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 10 from patent US 5783665.
ACCESSION      AR019521
VERSION      AR019521.1 GI:3974635
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 1317)
AUTHORS
  Baum, P. R., Fanslow, W. C. III, Gayle, R. B. and Goodwin, R. G.
TITLE
  Cytokine which is a ligand for OX40
JOURNAL
  Patent: US 5783665-A 10 21-JUL-1998;
FEATURES
  source
    1.1317
    /organism="unknown"
BASE COUNT      322 a      417 c      337 g      241 t
ORIGIN

Query Match      2.6%; Score 28; DB 6; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy 424 acaaccagcctgcaagcctgaccaa 451
Db 404 ACAACCAAGCCTGCAGCCCTGACCAA 431

RESULT 19
LOCUS 114936 1317 bp DNA linear PAT 02-APR-1996
DEFINITION Sequence 10 from patent US 5457035.
ACCESSION 114936
VERSION 114936.1 GI:1249844
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1317)
AUTHORS Baum,P.R., Fanslow,W.C. III, Gayle,R.B. and Goodwin,R.G.
TITLE Cyclokin which is a ligand for OX40
JOURNAL Patent: US 5457035-A 10 10-OCT-1995;
FEATURES
source 1..1317
/organism="Unknown"
BASE COUNT 322 a 417 c 337 g 241 t
ORIGIN

Query Match 2.6%; Score 28; DB 6; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 424 acaaccagcctgcaagcctgaccaa 451
Db 404 ACAACCAAGCCTGCAGCCCTGACCAA 431

RESULT 20
MMDNNOX40
LOCUS 2907 bp DNA linear ROD 23-AUG-1995
DEFINITION M.musculus ox40 gene.
ACCESSION X85214
VERSION X85214.1 GI:732818
KEYWORDS OX40 gene.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 2907)
AUTHORS Birkeland,M.L., Copeland,N.G., Gilbert,D.J., Jenkins,N.A. and Barclay,A.N.
TITLE Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein
JOURNAL Eur. J. Immunol. 25 (4), 926-930 (1995)
MEDLINE 95255413
REFERENCE 2 (bases 1 to 2907)
AUTHORS Birkeland,M.L.
TITLE Direct Submission
JOURNAL Submitted (10-MAR-1995) M.L. Birkeland, University of Pennsylvania, School of Medicine, 535 Clinical Research Building, 415 Curie Blvd., Philadelphia PA 19103, USA
COMMENT Sequence overlapping with that under the acc#221674.
FEATURES
location/Qualifiers
1..2907
/organism="Mus musculus"
/db_xref="taxon:10090"
join(<1..312,534..656,1208..1315,1692..1758,2196..2392,2472..2591,2680..2907)
<1..312
/number=1
join(180..312,534..656,1208..1315,1692..1758,2196..2392,2472..2591,2680..2750)
/gene="ox40"
join(180..312,534..656,1208..1315,1692..1758,2196..2392,2472..2591,2680..2750)

CDS

/gene="ox40"
/codon_start=1
/protein_id="CA59476.1"
/db_xref="GI:732819"
/db_xref="MGD:MGI:104512"
/db_xref="SWISS-PROT:P47741"
/translation="MYVWQDPTALLGLTGLGYTARLNCVKHTYPSGKRCRCQPGHGWASRCDHTRDITLCHPCETGFYNEAVNYDTCKQCTGCHNRSGSELKONCTPTODIVCRCRPGQPRQDSCGKLGVDVCPQPGHSPGNQACKPMYNTLTSGKQTRHPPASDSLDAVCEDRSLATFLMERTORPFRFRPTVSTYVMYRPSLSLPSPTLYTEGPAFVLLSLGLGLAPLTVALYTLRKAMRLPNTYKPCMGNSFRPIQEHDAHFTLAKI"
313..533
/gene="ox40"
/number=1
534..656
/gene="ox40"
/number=2
657..1207
/gene="ox40"
/number=2
1208..1315
/gene="ox40"
/number=3
1316..1691
/gene="ox40"
/number=3
1692..1758
/gene="ox40"
/number=4
1759..2195
/gene="ox40"
/number=4
2196..2392
/gene="ox40"
/number=5
2393..2471
/gene="ox40"
/number=5
2472..2591
/gene="ox40"
/number=6
2592..2679
/gene="ox40"
/number=6
2680..2907
/number=7
polyA_signal 2895..2900
BASE COUNT 688 a 755 c 776 g 688 t
ORIGIN

Query Match 2.6%; Score 28; DB 10; Length 2907;
Best Local Similarity 100.0%; Pred. No. 0.0062;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 424 acaaccagcctgcaagcctgaccaa 451
Db 1731 ACAACCAAGCCTGCAGCCCTGACCAA 1758

RESULT 21
AC100470/c 60953 bp DNA linear HTG 22-NOV-2001
LOCUS AC100470
DEFINITION Mus musculus clone RP23-139J18, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC100470
VERSION AC100470.1 GI:17047836
KEYWORDS HTG; HTGS_PHASE0.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE 1 (bases 1 to 60953)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE
JOURNAL
REFERENCE
AUTHORS

Mus musculus, clone RP23-139J18
Unpublished
2 (bases 1 to 60953)
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barnes, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,
Brown, A., Camarata, J., Campolano, A., Chang, J., Chazaro, B.,
Chapel, Y., Colangelo, M., Collins, S., Collamore, A., Cook, A.,
Cooper, P., DeRellano, K., Dewar, K., Diaz, U. S., Dodge, S., Ferro, S.,
Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Heatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Jones, C., Kamat, A., Karatas, A., Kells, C., Larocque, K.,
Lamarez, R., Lander, T., Lechoczy, J., Levine, R., Liu, G.,
Maclean, C., MacDonald, P., Major, J., Margulis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., McPheters, R., Meldrum, J.,
Menusz, L., Milnova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C.,
Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliyer, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schnupack, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigglio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center -----
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: I15392
Center clone name: 139_J_18

----- NOTE: This record contains 75 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

1
* 703 802: contig of 702 bp in length
* 803 1518: contig of 716 bp in length
* 1519 1618: gap of 100 bp
* 1619 2337: contig of 719 bp in length
* 2338 2437: gap of 100 bp
* 2438 3141: contig of 704 bp in length
* 3142 3241: gap of 100 bp
* 3242 3940: contig of 699 bp in length
* 3941 4040: gap of 100 bp
* 4041 4751: contig of 711 bp in length
* 4752 4851: gap of 100 bp
* 4852 5561: contig of 710 bp in length
* 5562 5661: gap of 100 bp
* 5662 6373: contig of 712 bp in length
* 6374 6473: gap of 100 bp
* 6474 7193: contig of 720 bp in length
* 7194 7293: gap of 100 bp
* 7294 8009: contig of 716 bp in length
* 8010 8109: gap of 100 bp
* 8110 8802: contig of 693 bp in length
* 8803 8902: gap of 100 bp

8903 9624: contig of 722 bp in length
* 9625 9724: gap of 100 bp
* 9725 10445: contig of 721 bp in length
* 10446 10545: gap of 100 bp
* 10546 11263: contig of 718 bp in length
* 11264 11363: gap of 100 bp
* 11364 12072: contig of 709 bp in length
* 12073 12172: gap of 100 bp
* 12173 12854: contig of 682 bp in length
* 12855 12954: gap of 100 bp
* 12955 13673: contig of 719 bp in length
* 13674 13773: gap of 100 bp
* 13774 14492: contig of 719 bp in length
* 14493 14592: gap of 100 bp
* 14593 15303: contig of 711 bp in length
* 15304 15403: gap of 100 bp
* 15404 16120: contig of 717 bp in length
* 16121 16220: gap of 100 bp
* 16221 16917: contig of 697 bp in length
* 16918 17017: gap of 100 bp
* 17018 17727: contig of 710 bp in length
* 17728 17827: gap of 100 bp
* 17828 18550: contig of 723 bp in length
* 18551 18650: gap of 100 bp
* 18651 19370: contig of 720 bp in length
* 19371 19470: gap of 100 bp
* 19471 20166: contig of 696 bp in length
* 20167 20266: gap of 100 bp
* 20267 20945: contig of 679 bp in length
* 20946 21045: gap of 100 bp
* 21046 21768: contig of 723 bp in length
* 21769 21868: gap of 100 bp
* 21869 22596: contig of 728 bp in length
* 22597 22696: gap of 100 bp
* 22697 23429: contig of 733 bp in length
* 23430 23529: gap of 100 bp
* 23530 24256: contig of 727 bp in length
* 24257 24356: gap of 100 bp
* 24357 25072: contig of 716 bp in length
* 25073 25172: gap of 100 bp
* 25173 25871: contig of 699 bp in length
* 25872 25971: gap of 100 bp
* 25972 26665: contig of 694 bp in length
* 26666 26765: gap of 100 bp
* 26766 27465: contig of 700 bp in length
* 27466 27565: gap of 100 bp
* 27566 28288: contig of 723 bp in length
* 28289 28388: gap of 100 bp
* 28389 29118: contig of 730 bp in length
* 29119 29218: gap of 100 bp
* 29219 29951: contig of 733 bp in length
* 29952 30051: gap of 100 bp
* 30052 30770: contig of 719 bp in length
* 30771 30870: gap of 100 bp
* 30871 31584: contig of 714 bp in length
* 31585 31684: gap of 100 bp
* 31685 32382: contig of 698 bp in length
* 32383 32482: gap of 100 bp
* 32483 33190: contig of 708 bp in length
* 33191 33290: gap of 100 bp
* 33291 33966: contig of 706 bp in length
* 33967 34096: gap of 100 bp
* 34097 34814: contig of 718 bp in length
* 34815 34914: gap of 100 bp
* 34915 35630: contig of 716 bp in length
* 35631 35730: gap of 100 bp
* 35731 36463: contig of 733 bp in length
* 36464 36563: gap of 100 bp
* 36564 37291: contig of 728 bp in length
* 37292 37391: gap of 100 bp
* 37392 38114: contig of 723 bp in length
* 38115 38214: gap of 100 bp
* 38215 38953: contig of 739 bp in length

```

* 38954 39053: gap of 100 bp
* 39054 39779: contig of 726 bp in length
* 39780 39879: gap of 100 bp
* 39880 40588: contig of 709 bp in length
* 40589 40688: gap of 100 bp
* 40689 41386: contig of 698 bp in length
* 41387 41486: gap of 100 bp
* 41487 42162: contig of 676 bp in length
* 42163 42262: gap of 100 bp
* 42263 42983: contig of 721 bp in length
* 42984 43083: gap of 100 bp
* 43084 43809: contig of 726 bp in length
* 43810 43909: gap of 100 bp
* 43910 44634: contig of 725 bp in length
* 44635 44734: gap of 100 bp
* 44735 45461: contig of 727 bp in length
* 45462 45561: gap of 100 bp
* 45562 46280: contig of 719 bp in length
* 46281 46380: gap of 100 bp
* 46381 47104: contig of 724 bp in length
* 47105 47204: gap of 100 bp
* 47205 47912: contig of 708 bp in length
* 47913 48012: gap of 100 bp
* 48013 48713: contig of 701 bp in length
* 48714 48813: gap of 100 bp
* 48814 49506: contig of 693 bp in length
* 49507 49606: gap of 100 bp
* 49607 50333: contig of 727 bp in length
* 50334 50433: gap of 100 bp
* 50434 51151: contig of 718 bp in length
* 51152 51251: gap of 100 bp
* 51252 51977: contig of 726 bp in length
* 51978 52077: gap of 100 bp
* 52078 52796: contig of 719 bp in length
* 52797 52896: gap of 100 bp
* 52897 53617: contig of 721 bp in length
* 53618 53717: gap of 100 bp
* 53718 54419: contig of 702 bp in length
* 54420 54519: gap of 100 bp
* 54520 55229: contig of 710 bp in length
* 55230 55329: gap of 100 bp
* 55330 56023: contig of 694 bp in length
* 56024 56123: gap of 100 bp

```

Query Match 2.6%; Score 28; DB 2; Length 60953;
 Best Local Similarity 100.0%; Pred. No. 0.0041;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 acaaccagcctgcaagcctgaccacaa 451
 Db 30950 ACAACCAAGCCTGCACAGCCCTGACCAA 30923

RESULT 22
 AL627204 253111 bp DNA linear HTG 27-OCT-2001
 LOCUS
 DEFINITION Mus musculus chromosome 4 clone RP23-118E21, *** SEQUENCING IN
 PROGRESS ***, in unordered pieces.
 ACCESSION AL627204.5 GI:16596721
 VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Direct Submission
 TITLE Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
 JOURNAL CB10 15A, UK. E-mail enquiries: humquery@sanger.ac.uk
 On Nov 2, 2001 this sequence version replaced gi:16416310.
 COMMENT
 ----- Genome Center

Center: Sanger Centre
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: bm118E21
 ----- Summary Statistics
 Sequencing program: XGAP4; version 4.5
 Sequencing vector: plasmid: 108752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 250604 bases at least Q40
 Consensus quality: 251169 bases at least Q30
 Consensus quality: 251526 bases at least Q20
 Insert size: 252011; sum-of-contigs
 Insert size: 263925; 8.0% error; agarose-fp
 Quality coverage: 11.85x in Q20 bases; sum-of-contigs quality
 coverage: 11.37x in Q20 bases; agarose-fp

 * NOTE: This is a 'working draft' sequence.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

FEATURES

source

Location/Qualifiers
 1..253111
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /chromosome="4"
 /clone="RP23-118E21"
 /clone_1lb="RPCT-23"
 1..23621
 /note="assembly_fragment:05628
 fragment_chain:1
 clone_end:SP6
 vector_side:left"
 23722..26584
 /note="assembly_fragment:07355
 fragment_chain:1"
 26685..32762
 /note="assembly_fragment:04295
 fragment_chain:1"
 32863..56771
 /note="assembly_fragment:00235
 fragment_chain:2"
 56872..61315
 /note="assembly_fragment:01898
 fragment_chain:2"
 61416..124554
 /note="assembly_fragment:02677
 fragment_chain:2"
 124655..138457
 /note="assembly_fragment:00397
 fragment_chain:2"
 138558..179038
 /note="assembly_fragment:00567
 fragment_chain:2"
 179139..210421
 /note="assembly_fragment:00017
 fragment_chain:2"
 210522..224019
 /note="assembly_fragment:07085
 fragment_chain:2"
 224120..227775
 /note="assembly_fragment:01289
 fragment_chain:3"
 227876..253111
 /note="assembly_fragment:03553
 fragment_chain:3
 clone_end:77
 vector_side:right"
 misc_count 65488 a 61670 c 60569 g 64276 t 1108 others

BASE COUNT 65488 a 61670 c 60569 g 64276 t 1108 others
 ORIGIN

Query Match 2.6%; Score 28; DB 2; Length 253111;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 424 acaccagcctgcgaagcctggaccac 451
Db 80147 ACACCAAGCCTGCAAGCCTGGACCA 80174

RESULT 23
AF389853 254197 bp DNA linear HTG 24-JAN-2002
LOCUS Mus musculus chromosome 4 clone RPCI-23-118E21 strain C57BL/6J,
DEFINITION WORKING DRAFT SEQUENCE, 13 ordered pieces.
ACCESSION AF389853
VERSION AF389853.1 GI:18307770
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 254197)
AUTHORS Li,X., Bachmanov,A.A., Li,S., Chen,Z., Tordoff,M.G.,
Beauchamp,G.K., de Jong,P.J., Wu,C., Chen,L., West,D.B., Ross,D.A.,
Ohmen,J.D. and Reed,D.R.
TITLE Genetic, physical, and comparative map of the subtelomeric region
of mouse chromosome 4
JOURNAL Mamm. Genome 13 (1), 5-19 (2002)
MEDLINE 21635547
PUBMED 11773963
REFERENCE 2 (bases 1 to 254197)
AUTHORS Reed,D.R., Li,X., Bachmanov,A.A., Li,S., Chen,Z., Tordoff,M.G.,
Beauchamp,G.K., de Jong,P.J., Wu,C., Chen,L., West,D.B., Ross,D.A.
and Ohmen,J.D.
TITLE Direct Submission
JOURNAL Submitted (08-JUN-2001) Monell Chemical Senses Center, 3500 Market
St, Philadelphia, PA 19104, USA
COMMENT * NOTE: This is a 'working draft' sequence. It currently
* consists of 13 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 32448: contig of 32448 bp in length
* 32449 32548: gap of unknown length
* 32549 56900: contig of 24352 bp in length
* 56901 57000: gap of unknown length
* 57001 115350: contig of 58350 bp in length
* 115351 115450: gap of unknown length
* 115451 118046: contig of 2596 bp in length
* 118047 118146: gap of unknown length
* 118147 123765: contig of 5619 bp in length
* 123766 123865: gap of unknown length
* 123866 124811: contig of 946 bp in length
* 124812 124911: gap of unknown length
* 124912 132352: contig of 7341 bp in length
* 132353 132352: gap of unknown length
* 132353 154052: contig of 21700 bp in length
* 154053 154152: gap of unknown length
* 154153 183134: contig of 28982 bp in length
* 183135 183234: gap of unknown length
* 183235 197716: contig of 14482 bp in length
* 197717 223095: contig of 25279 bp in length
* 223096 223195: gap of unknown length
* 223196 227717: contig of 4522 bp in length
* 227718 227817: gap of unknown length
* 227818 254197: contig of 26380 bp in length.
FEATURES
source 1..254197
Location/Qualifiers

/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/chromosome="4"
/clone="RPCI-23-118E21"
BASE COUNT 62796 a 60035 c 62871 g 67274 t 1221 others
ORIGIN

Query Match 2.6%; Score 28; DB 2; Length 254197;
Best Local Similarity 100.0%; Pred. No. 0.0034;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 424 acaccagcctgcgaagcctggaccac 451
Db 201227 ACACCAAGCCTGCAAGCCTGGACCA 201254

RESULT 24
AX251339 5148 bp DNA linear PAT 05-OCT-2001
LOCUS Sequence 307 from Patent WO0168912.
DEFINITION AX251339
ACCESSION AX251339
VERSION AX251339.1 GI:15984762
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 5148)
AUTHORS Olek,A., Piepenbrock,C. and Berlin,K.
TITLE Diagnosis of diseases associated with tumor suppressor genes and
oncogenes
JOURNAL Patent: WO 0168912-A 307 20-SEP-2001;
EpiGenomics AG (DE)
FEATURES
source 1..5148
Location/Qualifiers
1..5148
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="Chemically treated genomic DNA (Homo sapiens)"
BASE COUNT 871 a 182 c 1479 g 2615 t 1 others
ORIGIN
Query Match 2.2%; Score 23; DB 6; Length 5148;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 5 agagacgagatgcgtcg999 27
Db 4796 AGAGACGAGATGCGTGGCGG 4818

RESULT 25
AC007905 104480 bp DNA linear HTG 03-OCT-2000
LOCUS Homo sapiens chromosome 16q24.3 clone RP4-754F23, WORKING DRAFT
DEFINITION SEQUENCE, 35 ordered pieces.
ACCESSION AC007905
VERSION AC007905.2 GI:10280722
KEYWORDS HTG; HTGS_PHASE2; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 104480)
AUTHORS Kremmidiotis,G., Gardner,A.E., Callen,D.F. and Sutherland,G.R.
TITLE Large Scale Sequencing of the Chromosome 16 region q24.3
JOURNAL unpublished
REFERENCE 2 (bases 1 to 104480)
AUTHORS Kremmidiotis,G., Gardner,A.E., Callen,D.F. and Sutherland,G.R.
TITLE Direct Submission
JOURNAL Submitted (24-JUN-1999) Cytogenetics & Molecular Genetics, Women's
& Children's Hospital, 72 King William Rd, Adelaide, SA 5006,

COMMENT

Australia
On Sep 23, 2000 this sequence version replaced gi:5174819.

Genome Centre : CytoGenetics & Molecular Genetics
Centre Code : CMGMCH
Website: <http://www.wch.sa.gov.au/labmedic/genetics/sequencing.html>

* NOTE: This is a 'working draft' sequence. It currently
* consists of 35 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 1479: contig of 1479 bp in length
* 1480 1487: gap of unknown length
* 1488 6699: contig of 5212 bp in length
* 6700 6707: gap of unknown length
* 6708 10905: contig of 4198 bp in length
* 10906 10912: gap of unknown length
* 10913 11733: contig of 821 bp in length
* 11734 11740: gap of unknown length
* 11741 12602: contig of 862 bp in length
* 12603 12609: gap of unknown length
* 12610 13856: contig of 1247 bp in length
* 13857 13863: gap of unknown length
* 13864 20018: contig of 6155 bp in length
* 20019 20025: gap of unknown length
* 20026 21942: contig of 1917 bp in length
* 21943 21949: gap of unknown length
* 21950 23920: contig of 1971 bp in length
* 23921 23927: gap of unknown length
* 23928 24860: contig of 933 bp in length
* 24861 24867: gap of unknown length
* 24868 29279: contig of 4412 bp in length
* 29280 29286: gap of unknown length
* 29287 29772: contig of 486 bp in length
* 29773 29779: gap of unknown length
* 29780 32411: contig of 2632 bp in length
* 32412 32418: gap of unknown length
* 32419 33145: contig of 727 bp in length
* 33146 33152: gap of unknown length
* 33153 34862: contig of 1710 bp in length
* 34863 34869: gap of unknown length
* 34870 36643: contig of 1774 bp in length
* 36644 36650: gap of unknown length
* 36651 37348: contig of 698 bp in length
* 37349 37355: gap of unknown length
* 37356 42174: contig of 4819 bp in length
* 42175 42182: gap of unknown length
* 42183 45604: contig of 3423 bp in length
* 45605 45611: gap of unknown length
* 45612 48485: contig of 2874 bp in length
* 48486 48492: gap of unknown length
* 48493 49845: contig of 1353 bp in length
* 49846 49852: gap of unknown length
* 49853 51199: contig of 1347 bp in length
* 51200 51206: gap of unknown length
* 51207 51513: contig of 307 bp in length
* 51514 51520: gap of unknown length
* 51521 52180: contig of 660 bp in length
* 52181 52187: gap of unknown length
* 52188 60026: contig of 7839 bp in length
* 60027 60033: gap of unknown length
* 60034 64699: contig of 4666 bp in length
* 64700 64706: gap of unknown length
* 64707 69136: contig of 4430 bp in length
* 69137 69143: gap of unknown length
* 69144 73347: contig of 4204 bp in length
* 73348 73354: gap of unknown length
* 73355 82462: contig of 9108 bp in length

* 82463 82469: gap of unknown length
* 82470 84166: contig of 1697 bp in length
* 84167 84173: gap of unknown length
* 84174 84822: contig of 649 bp in length
* 84823 84829: gap of unknown length
* 84830 99511: contig of 14682 bp in length
* 99512 99518: gap of unknown length
* 99519 101087: contig of 1569 bp in length
* 101088 101094: gap of unknown length
* 101095 103316: contig of 2222 bp in length
* 103317 103323: gap of unknown length
* 103324 104480: contig of 1157 bp in length.

FEATURES
source
1..104480
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="16q24.3"
/clone="RP4-754F23"

BASE COUNT 23140 a 28756 c 29631 g 22706 t 247 others
ORIGIN
Query Match 2.2%; Score 23; DB 2; Length 104480;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 671 ggagctggagcctgctgctggagc 693
|||||
Db 6816 GGCCCTGGGCTGCTGCTGGGC 6838

RESULT 26
AB003911 877 bp mRNA linear MAM 05-FEB-1999
LOCUS
DEFINITION Rabbit mRNA for OX40 precursor, partial cds.
ACCESSION AB003911
VERSION AB003911.1 GI:2114107
KEYWORDS OX40.
SOURCE Oryctolagus cuniculus (sub_species:domesticus, strain:Chdb:HM)
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
AUTHORS Isono, T.
TITLE Direct Submission
JOURNAL Submitted (14-MAY-1997) Takahiro Isono, Shiga University of Medical
Science, Central Research Laboratory, Seta Tsukinowachou, Otsu,
Shiga 520-2192, Japan (E-mail: isono@belle.shiga-med.ac.jp,
Tel:81-775-48-2308, Fax:81-775-48-2048)
2 (sites)
REFERENCE
AUTHORS Isono, T. and Seto, A.
TITLE Expression of OX40 and OX40 ligand genes in rabbit
HTLV-I-transformed T cell lines
JOURNAL HTLV-I-transformed T cell lines
FEATURES
Unpublished (1997)
source
1..877
Location/Qualifiers
/organism="Oryctolagus cuniculus"
/strain="Chdb:HM"
/sub_species="domesticus"
/db_xref="taxon:9986"
/cell_line="H446"
/cell_type="HTLV-I-transformed T cell"
1..54
1..804
/codon_start=1
/product="OX40 precursor"
/protein_id="BAA20059.1"
/db_xref="GI:2114108"
/translation="GLAALGIALILGILGAEPRPCVGDPTYPGGRRCLEQPGY
GVNSRCNSODPIICHPCEGRFENAVNYOACKPCQCKRRSSSEQDCTHTRDYCR
CRPGTPLNGTKHGVDCAPCQGHFSEGNRRACRWITCTLAGKTLQAPASSISAVC
EDRSSLATQPWETPSAPYRPPARTSTAMPRTAQPSPPTLEASKGPDLAIVLSIGLG

mat_peptide LGLLALLAALLALYHQRAMRPPKLPGGSEFTPIQEQDAGSTMAKT"
55. .801
/product="OX40"

BASE COUNT 157 a 324 c 275 g 121 t
ORIGIN

Query Match 2.0%; Score 21; DB 4; Length 877;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 440 gccctggaccactgcacct 460
Db 408 GCCCTGGACCACTGCACCTT 428

RESULT 27
LOCUS BC002494 1420 bp mRNA linear PRI 12-JUL-2001
DEFINITION Homo sapiens, clone IMAGE:3050476, mRNA, partial cds.
ACCESSION BC002494
VERSION BC002494.1 GI:12803350
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 1420)
JOURNAL Strausberg, R.
Direct Submision
Submitted (05-FEB-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgabs-remail.nih.gov
Tissue Procurement: ATCC/DCRD/PTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nrl.nih.gov

Shevchenko, Y., Wetherby, K.D., Beckstrom-Sternberg, S.M.,
Benjamin, B., Blakesley, R.W., Boufard, G.G., Brinkley, C., Brooks, S.,
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
Lim, M., Maduro, Q.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Snyder, B., Starikoff, S., Thomas, P.J.,
Tlonsong, E.E., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A.,
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov
Series: IRAL Plate: 4 Row: e Column: 1
This clone was selected for full length sequencing because it
passed the following selection criteria: Genomescan gene
prediction.

FEATURES
source
1. .1420
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3050476"
/issue_type="Skin, melanotic melanoma."
/clone_lib="NIH-MGC-20"
/lab_host="DH10B-R"
/note="Vector: pOTB7"
<1. .1084
/codon_start=2
/product="Unknown (protein for IMAGE:3050476)"
/protein_id="AAH02494.1"
/db_xref="GI:12803351"

CDS

/translation="ARGASRGGLGVSNAMESTLIGACIVIAEALQNLAMLENVIMLT
FLGDPKILFLFFPAAYVASRRVGLVILWISLITELNLIFFWFLFGDRPFVWVHS
YSSOAPAOVHOFPSSECTGPGSPGCHMTGAALMIMTALSSQVATRRASRVVMP
SLAVCFELAVGLSRFIFLAHPHOVLACILGAVIGMTMPRPAPERELSFGLTAL
ALMGSLIYKTLFTLGLDLSMSISLAFWCRCRPRRIVHDSRPAFSLSDSCAALGIG
IALHSPCAQVRAOLGNGCKTACILVLANGLLGLPDLMLGHPPOISLFTIFNFKITLW
PCLVLALVMAVMEFSAQEPPIHSS"

Query Match 2.0%; Score 21; DB 9; Length 1420;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 688 tggggtctgctggccccctgg 708
Db 915 TGGGGCTGCTGGCCCCCTGG 935

RESULT 28
LOCUS AX202231 1569 bp DNA linear PAT 30-AUG-2001
DEFINITION Sequence 10 from Patent WO0153469.
ACCESSION AX202231
VERSION AX202231.1 GI:15392005
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 1569)
JOURNAL Bandman, O., Tang, Y.T., Azimzai, Y., Yue, H., Baughn, M.R.,
Hillman, J.L., Lal, P., Wang, E., Gandhi, A.R., Policky, J.L. and
Mathur, P.
Phosphatases
Patent: WO 0153469-A 10-26-JUL-2001;
Incyte Genomics, Inc. (US)

FEATURES
source
1. .1569
/organism="Homo sapiens"
/db_xref="taxon:9606"
/note="Incyte ID No: 1269556CB1"

BASE COUNT 263 a 505 c 444 g 357 t
ORIGIN

Query Match 2.0%; Score 21; DB 6; Length 1569;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 688 tggggtctgctggccccctgg 708
Db 1089 TGGGGCTGCTGGCCCCCTGG 1109

RESULT 29
LOCUS HSM802071 1632 bp mRNA linear PRI 18-FEB-2000
DEFINITION Homo sapiens mRNA; CDNA DKFZp434L1226 (from clone DKFZp434L1226).
ACCESSION AL137382
VERSION AL137382.1 GI:6807912
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
TITLE 1 (bases 1 to 1632)
JOURNAL Ansoorge, W., Wilkner, U., Mewes, H.W., Weil, B. and Wiemann, S.
Direct Submision
Submitted (15-JAN-2000) MIPS, Am Klopferplatz 18a, D-82152
Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFZp434L1226) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

FEATURES

SOURCE

Location/Qualifiers

```

1. 1632
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="DKFZp434L1226"
  /clone_id="434 (synonym: htes3). Vector pSport1; host
  DH10B; sites NotI + SalI"
  /dev_stage="adult"
  /tissue_type="testis"
  /map="16q24.3"
BASE COUNT      282 a      528 c      489 g      333 t
ORIGIN

```

Query Match 2.0%; Score 21; DB 9; Length 1632;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 672 ggccgtggccgtgtgtcgtg 692
|||||
Db 1006 GGCCTGGGCTGTGTCTGGGG 1026

RESULT 30

LOCUS BC021574 1634 bp mRNA linear PRI 18-JAN-2002
DEFINITION Homo sapiens, clone MGC:31975 IMAGE:4842511, mRNA, complete cds.
ACCESSION BC021574
VERSION BC021574.1 GI:18204314
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1634)
Strausberg, R.
Direct Submission
Submitted (14-JAN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,
Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,
Leticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo
Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven
Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline
Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,
Michael Thorne, Miranada Tsai, Natassja van den Bosch, Jill Vardy,
George Yang, Scott Zuyderduyn, Marco Marra.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 40 Row: 1 Column: 5
This clone was selected for full length sequencing because it
passed the following selection criteria: Hexamer frequency OKF

analysis, Genomescan gene prediction.

FEATURES

SOURCE

Location/Qualifiers

CDS

```

1. 1634
  /organism="Homo sapiens"
  /db_xref="taxon:9606"
  /clone="MGC:31975 IMAGE:4842511"
  /tissue_type="Eye, normal, pigmented retinal epithelium"
  /clone_id="NIH-MGC_43"
  /lab_host="DH10B-R"
  /note="Vector: pORF7"
  217. 1257
  /codon_start=1
  /product="Unknown (protein for MGC:31975)"
  /protein_id="AAH21574.1"
  /db_xref="GI:18204315"
  /translation="MESLGLGVIYAELQNLAMLENNVIMTIFGDPKTLFLFYP
  AAYASRRVGIATVLMISLITFELNLFELFEGDPRFVWVHESGYSAPAVQHPFS
  SCETGPGSPSGCHMITGAAMPIMTALSSOYATRASRNVMPSLACTFLAVGLS
  RIFLIARPHQVLGLITGAVLVGLMTPRVMERELSFYGLTALALMGSTLIYWTLE
  TLGLDLSWSISLAFKMCERPEMIVHSRPFASLSRDSGALGLIALHSPCYAQRRA
  QLNGOKTACVLAMGLGLGPIQISLFYIFNFKYTLMPCLALVPAVYHA
  FSAQEARPIHSS"
BASE COUNT      330 a      502 c      444 g      358 t
ORIGIN

```

Query Match 2.0%; Score 21; DB 9; Length 1634;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 688 tgggctgtctggcccttg 708
|||||
Db 1088 TGGGCTGTCTGGGCCCTTGG 1108

Search completed: June 19, 2002, 02:21:10
Job time: 3946 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:11:59 ; Search time 1591.56 Seconds
(without alignments)
8972.190 Million cell updates/sec

Title: US-09-852-845-1
Perfect score: 1058
Sequence: 1 cagcagagcagcagatgtc.....cacataaaaccttgcag 1058

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 13736207 seqs, 6748477542 residues

Word size : 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database :

EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estlin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estio:*
8: em_hlc:*
9: gb_estl:*
10: gb_est2:*
11: gb_hlc:*
12: gb_gss:*
13: em_gss_hum:*
14: em_gss_inv:*
15: em_gss_pln:*
16: em_gss_vrt:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	431	40.7	569	10	BG236062 naft2a07.
2	391	37.0	544	10	BF063899 7f90a10.x
3	386	36.5	512	10	BE349098 ht50905.x
4	256	24.2	844	9	A1738634 w11d02.x
5	240	22.7	393	9	AA306055 EST177040
6	229	21.6	471	9	AA293499 UI-H-BI2-
7	207	19.6	353	9	AM290885 UI-H-BI2-
8	203	19.2	743	10	BI833441 603088095
9	171	16.2	198	9	AM591834 xx68b03.x
10	142	13.4	172	10	BI824093 603039230
11	110	10.4	893	10	BI911081 603069733
12	94	8.9	347	9	A1452801 t350f10.x
13	92	8.7	92	10	BI821828 603035715
14	82	7.8	398	9	AA970291 op09h05.s
15	58	5.5	247	9	AI914208 wd76e10.x
16	45	4.3	668	9	AI991307 wd2d05.x
17	28	2.6	662	12	A2320958 IM0041A08

18	24	2.3	630	9	AA501118 v197h05.r
19	21	2.0	342	9	AM889471 RC6-NT002
20	21	2.0	477	9	AI823620 w171d07.x
21	21	2.0	480	9	AA312871 EST183529
22	21	2.0	482	9	AI126122 qd77b04.x
23	21	2.0	545	9	AA477725 z044f11.s
24	21	2.0	572	9	AL523655 AL523655
25	21	2.0	585	10	BF810986 CM2-C1017
26	21	2.0	636	9	AI264358 q109f04.x
27	21	2.0	649	9	AI669655 wcl2a05.x
28	21	2.0	650	10	BM006189 603614011
29	21	2.0	653	10	BF725110 bx12c11.y
30	21	2.0	683	10	BG422683 602449189
31	21	2.0	692	10	BF036463 601460214
32	21	2.0	736	9	AL578769 AL578769
33	21	2.0	755	9	AL524354 AL524354
34	21	2.0	759	10	BI258768 602970353
35	21	2.0	762	10	BE312775 601149543
36	21	2.0	774	10	BM048374 603625618
37	21	2.0	779	10	BG478742 602525664
38	21	2.0	789	9	AL572583 AL572583
39	21	2.0	790	10	BG479022 602525793
40	21	2.0	799	10	BI871312 603392733
41	21	2.0	805	10	BM042047 603616048
42	21	2.0	820	9	AL526414 AL526414
43	21	2.0	827	9	AL578318 AL578318
44	21	2.0	834	10	BF314033 601901472
45	21	2.0	842	10	BG750265 602709068
46	21	2.0	845	10	BG474551 602517325
47	21	2.0	851	9	AL533389 AL533389
48	21	2.0	854	9	AL524355 AL524355
49	21	2.0	857	9	AL521417 AL521417
50	21	2.0	864	9	AL521416 AL521416

ALIGNMENTS

RESULT 1
LOCUS BG236062/c 569 bp mRNA linear EST 12-FEB-2001
DEFINITION naft2a07.x1 Soares,NPBC Homo sapiens CDNA clone IMAGE:4141716 3'
similar to SW:OX40.HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains
MER22.cl TARI repetitive element ;, mRNA sequence.

ACCESSION BG236062
VERSION BG236062
KEYWORDS
SOURCE
ORGANISM

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 569)
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE
Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D. and M. Fatima
Bonaldo, Ph.D.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CCAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNLN at:
InfoImage.lnl.gov
Seq primer: -400P from Glibco
High quality sequence stop: 478.
location/Qualifiers
1. 569

FEATURES

source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4141716"

```

/clone_1lb="Soares_NFBMC"
/tissue_type="lymphocyte"
/lab_host="DH10B (phage-resistant)"
/notice="organ: blood; Vector: pRT7D-Pac; Site_1: NotI;
Site_2: EcoRI; 1st strand cDNA was primed with a Not I -
oligo(dT) primer [5',
TGTTACCAATCTGAAGTGGGACGGCCGGGTTTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pRT73 vector. Library
is normalized; constructed in the laboratory of M. Bento
Soares (University of Iowa)."
```

Query Match	40.7%	Score 431	DB 10	Length 569
Best Local Similarity	99.8%	Pred. No.	2.6e-192	
Matches 551	Conservative 0	Mismatches 0	Indels 1	Gaps 1

QY	507	atctcttgagacaaaggaaaccccccaagcaagcagcccaaggaaacccaagagccccccgagc	566
Db	569	ATCTGTGAGAGCAAGGAGGACCCCCCAAGCCACGACGCCCAAGAGACCACGAGGCCCCCGGCC	510
QY	567	aggaccatcaactgtctcaagcccaactgaagcctctggtcccaagaacctcacaaggaacctccac	626
Db	509	AGGCCATTCACATGTCACACCCCACTGAAGCTGTGGCCAGAACCTCAGAGGACCTTCACAC	450
QY	627	cggcccgctggaagggtcccccggggggccgtcggtgtgcgcgaacctctggcccttggccttggt	686
Db	449	CGGCCCGTGAGAGTCCCGGGGGCGGTGCGGTGGCCATTCCTGGGCTGGGCGTGGTG	390
QY	687	ctggggcgtgcctggggcccccctgagcaacctgtctgtgcctcttaactgtctccgaaggagacag	746
Db	389	CTGGGGGCTGCTGAGGCCCCCTTGACATCTCTGTGCGCCCTGTACTCTCTCCGAGGAGACCA	330
QY	747	aggatgcctcccccagatgycaccaagaagcccccttggggagagagtlctccgaagcccccatcca	806
Db	329	AGGCTGCCCCCGAGATGCCACAAAGCCCCCTGGGGGAGGAGAGTTTCGGAGCCCCCATCCAA	270
QY	807	gagagacagagccgaagcccaatccaaacctgtgcgaagatctgaaccttgggcccaagaagt	866
Db	269	GAGGAGCAAGGCCGAGGCCACCTACCTCCCTGGGCAAGATCTGACC--TGGGGCCACCAAGAT	211
QY	867	ggaacactgagcccccgcgaaggctctggaagcccgaaagggtctgtcctbaggaggaagcaagggtgc	926
Db	210	GGACGCTGGGCCCCGCCCAAGGCTGAGGCCGAGGGGTCTGTCTGGGAGAGGGCAAGGTGC	151
QY	927	aggcgcacctgcgccgcgaagctctcctbaggagccaaacttgtacacglttctaaagtgcagatgct	986
Db	150	AGGCGGCTGGCCCCGCCCAAGGCTCTGGGGCAAACTGTGACGCTTCTAGGTGCGATGGGT	91
QY	987	gacctcggcgtctctgcttaagtaatgcatatgcatatacctccctgcgcccgaggacacaataa	1046
Db	90	GCGTCCGGGCTCTGTGCTTACGATGTCATGTGCTACTCTCTGCCCCGCGGAGACACAATAA	31
QY	1047	aaactctgacag	1058
Db	30	AAACTCTGGCAG	19

RESULT	2
BF063899/c	
LOCUS	BF063899
DEFINITION	7H9A10.X1 NCI-CGAP Co16 Homo sapiens cDNA clone IMAGE:332326 3'
	similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains
	MER22.tl PTR5 repetitive element ; , mRNA sequence.
ACCESSION	BF063899
VERSION	BF063899.1 GI:10822809
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
Mammalia: Eutheria; Primates; Carnivora; Hominoidea; Homo. 1 (bases 1 to 544) NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap .	
National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index	
Unpublished (1997)	
Contact: Robert Strausberg, Ph.D.	

Contact: Robert Strausberg, Ph.D.
Email: c9apbs-remail.nih.gov
Tissue Procurement: Ian Kirsch, M.D., Michael R. Emmert-Buck, M.D.
Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL, send email to:
info@image.lnl.gov

Seq primer: -400p from Glbco
High quality sequence stop: 423.

FEATURES
SOURCE

1.544

```
/ddb_xref="taxon:9606"
```

```
/clone lib=NCI CGAP CC
```

```

/issue_type="colon fun
/lab_host="DH10B"

```

```
/note="Organ: colon; Ve
```

Plasmid DNA from the no

purification, this DNA

hydrazalium reaction from a pool of 5,000 cells.

(cloneIDs 1057416-10612

a 167 c 216 g

37.08: Score 391

99.88; Pred. No.

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
84

CCCCC00CCAC1CAC1G

accclccaccgucclcgagga

ACCCCTCCACCCGGCCCGTGGAGGT

gggctgtgtgctgggctgctgg

GGGCTGGTGGCTGGGGCTGGCTGGC

[illegible]

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1

CCCCAICCAAGAGGACAGGCLCG

ccaccgaagtggacgctgggcc

CCACCAAGGTGGACGCTGGGCCCC

1. **Introduction**
 2. **Background**
 3. **Methodology**
 4. **Results**
 5. **Discussion**
 6. **Conclusion**
 7. **References**
 8. **Appendix**
 9. **Index**
 10. **Table of Contents**
 11. **Abstract**
 12. **Summary**
 13. **Key Words**
 14. **Keywords**
 15. **Subject Headings**
 16. **Classification**
 17. **Indexing**
 18. **References**
 19. **Appendix**
 20. **Index**
 21. **Table of Contents**
 22. **Abstract**
 23. **Summary**
 24. **Key Words**
 25. **Keywords**
 26. **Subject Headings**
 27. **Classification**
 28. **Indexing**
 29. **References**
 30. **Appendix**
 31. **Index**
 32. **Table of Contents**
 33. **Abstract**
 34. **Summary**
 35. **Key Words**
 36. **Keywords**
 37. **Subject Headings**
 38. **Classification**
 39. **Indexing**
 40. **References**
 41. **Appendix**
 42. **Index**
 43. **Table of Contents**
 44. **Abstract**
 45. **Summary**
 46. **Key Words**
 47. **Keywords**
 48. **Subject Headings**
 49. **Classification**
 50. **Indexing**
 51. **References**
 52. **Appendix**
 53. **Index**
 54. **Table of Contents**
 55. **Abstract**
 56. **Summary**
 57. **Key Words**
 58. **Keywords**
 59. **Subject Headings**
 60. **Classification**
 61. **Indexing**
 62. **References**
 63. **Appendix**
 64. **Index**
 65. **Table of Contents**
 66. **Abstract**
 67. **Summary**
 68. **Key Words**
 69. **Keywords**
 70. **Subject Headings**
 71. **Classification**
 72. **Indexing**
 73. **References**
 74. **Appendix**
 75. **Index**
 76. **Table of Contents**
 77. **Abstract**
 78. **Summary**
 79. **Key Words**
 80. **Keywords**
 81. **Subject Headings**
 82. **Classification**
 83. **Indexing**
 84. **References**
 85. **Appendix**
 86. **Index**
 87. **Table of Contents**
 88. **Abstract**
 89. **Summary**
 90. **Key Words**
 91. **Keywords**
 92. **Subject Headings**
 93. **Classification**
 94. **Indexing**
 95. **References**
 96. **Appendix**
 97. **Index**
 98. **Table of Contents**
 99. **Abstract**
 100. **Summary**
 101. **Key Words**
 102. **Keywords**
 103. **Subject Headings**
 104. **Classification**
 105. **Indexing**
 106. **References**
 107. **Appendix**
 108. **Index**
 109. **Table of Contents**
 110. **Abstract**
 111. **Summary**
 112. **Key Words**
 113. **Keywords**
 114. **Subject Headings**
 115. **Classification**
 116. **Indexing**
 117. **References**
 118. **Appendix**
 119. **Index**
 120. **Table of Contents**
 121. **Abstract**
 122. **Summary**
 123. **Key Words**
 124. **Keywords**
 125. **Subject Headings**
 126. **Classification**
 127. **Indexing**
 128. **References**
 129. **Appendix**
 130. **Index**
 131. **Table of Contents**
 132. **Abstract**
 133. **Summary**
 134. **Key Words**
 135. **Keywords**
 136. **Subject Headings**
 137. **Classification**
 138. **Indexing**
 139. **References**
 140. **Appendix**
 141. **Index**
 142. **Table of Contents**
 143. **Abstract**
 144. **Summary**
 145. **Key Words**
 146. **Keywords**
 147. **Subject Headings**
 148. **Classification**
 149. **Indexing**
 150. **References**
 151. **Appendix**
 152. **Index**
 153. **Table of Contents**
 154. **Abstract**
 155. **Summary**
 156. **Key Words**
 157. **Keywords**
 158. **Subject Headings**
 159. **Classification**
 160. **Indexing**
 161. **References**
 162. **Appendix**
 163. **Index**
 164. **Table of Contents**
 165. **Abstract**
 166. **Summary**
 167. **Key Words**
 168. **Keywords**
 169. **Subject Headings**
 170. **Classification**
 171. **Indexing**
 172. **References**
 173. **Appendix**
 174. **Index**
 175. **Table of Contents**
 176. **Abstract**
 177. **Summary**
 178. **Key Words**
 179. **Keywords**
 180. **Subject Headings**
 181. **Classification**
 182. **Indexing**
 183. **References**
 184. **Appendix**
 185. **Index**
 186. **Table of Contents**
 187. **Abstract**
 188. **Summary**
 189. **Key Words**
 190. **Keywords**
 191. **Subject Headings**
 192. **Classification**
 193. **Indexing**
 194. **References**
 195. **Appendix**
 196. **Index**
 197. **Table of Contents**
 198. **Abstract**
 199. **Summary**
 200. **Key Words**
 201. **Keywords**
 202. **Subject Headings**
 203. **Classification**
 204. **Indexing**
 205. **References**
 206. **Appendix**
 207. **Index**
 208. **Table of Contents**
 209. **Abstract**
 210. **Summary**
 211. **Key Words**
 212. **Keywords**
 213. **Subject Headings**
 214. **Classification**
 215. **Indexing**
 216. **References**
 217. **Appendix**
 218. **Index**
 219. **Table of Contents**
 220. **Abstract**
 221. **Summary**
 222. **Key Words**
 223. **Keywords**
 224. **Subject Headings**
 225. **Classification**
 226. **Indexing**
 227. **References**
 228. **Appendix**
 229. **Index**
 230. **Table of Contents**
 231. **Abstract**
 232. **Summary**
 233. **Key Words**
 234. **Keywords**
 235. **Subject Headings**
 236. **Classification**
 237. **Indexing**
 238. **References**
 239. **Appendix**
 240. **Index**
 241. **Table of Contents**
 242. **Abstract**
 243. **Summary**
 244. **Key Words**
 245. **Keywords**
 246. **Subject Headings**
 247. **Classification**
 248. **Indexing**
 249. **References**
 250. **Appendix**
 251. **Index**
 252. **Table of Contents**
 253. **Abstract</**

100

[illegible]

Dd	97	CCTTACGATGCCCATGGCCTGCCTCCCGCTCTCTTCATTAGCATGTGCATGCATACCCTCCT	38
Oy	1027	gccccgcggagcacacaataaaaccttgcacg	1058
Dd	37	GCCCCGCGGAGCACACAATAAAACTTGCGAG	6
RESULT	3		
BEST LOCAL LOCUS	BE349098/c		
DEFINITION		512 bp mRNA linear EST 18-JUL-2000	
VERSION	h550905.x1 NCI CGAP Mell15 Homo sapiens CDNA clone IMAGE:3150200.3'		
KEYWORDS	Similar to SW:OX4D_HUMAN P43489 OX4D RECEPTOR PRECURSOR ;contains MEN22.L1 PTRS repetitive element ; , mRNA sequence.		
SOURCE	BE349098		
ORGANISM	BE349098.1 GI:9261037		
REFERENCE	EST.		
AUTHORS	Homo sapiens		
TITLE	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap. National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cga@bs-re@mail.nih.gov Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life Technologies, Inc. CDNA library Arrayed by: Christina Prange, The I.M.A.G.E. Consortium DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LIML, send email to: info@image.liml.gov Seq primer: -40UP from Gibco High quality sequence stop: 427.		
FEATURES			
Source			
	Location/Qualifiers		
	1..512		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:3150200"		
	/clone_lib="NCI CGAP_Mel15"		
	/tissue_type="malignant melanoma, metastatic to lymph node"		
	/lab_host="DH10B"		
	/note="Organ: skin; Vector: PCMV-SPORT6; Site.1: SalI; Site.2: NotI; Cloned unidirectionally. Primer: oligo dT. Library constructed by Life Technologies."		
BASE COUNT	73 a 162 c 200 g 77 t		
ORIGIN			
Query Match		36.5%; Score 386; DB 10; Length 512;	
Best Local Similarity	99.8%; Pred. No. 4.2e-171;		
Matches	506; Conservative 0; Mismatches 0; Indels 1; Gaps 1;		
Oy	552	cagggcccccgcggcagaaccatctgtccagccactgaagccttggtcccaactcca	611
Dd	512	CAGGCGCCCCCGCGCAGGCGCACTGTCAGCCACAGGAAGCCTGGGCCAGAACCTTA	453
Oy	612	cagggaaccttcacaccgcgcgttagagtcccccggggcgcggtttgcgcgatctcg	671
Dd	452	CAGGGAACCTTCACCCGGCGCGCTGAGAGTCCCAGGGGCGCGTAGCATTTCCGCAATCCG	393
Oy	672	gacctgggccttgtctgtgggctgtgtgggcccccttgcatctactctgtgacctgtacctg	731
Dd	392	GGCGTGGGCGTGTGCTGTGGGCGCTGCTGGGCCCCCTGGCATTCCTGTGCGCCTGTACCTG	333
Oy	732	cctcggaagagacagagctgtcccccgatgtcccaaaaagcccccctggyggagagcaatttc	791
Dd	332	CTCCGAGAGGACCAAAGCTGTCCCCCGATGCTCCCAAGAAGCCCCCTGGGGAGGAGGATTTTC	273

QY	792	cgagaccatccatcaagagagacgagcgacgcccacccctccacccctgagccagatctgacct	851
Db	272	CGGACCCCCATTCACAGAGAGAGAGAGCCGACGCGCCACTCCACCTGGCCAAATCTGAC	212
QY	852	tgggcccacacaaaggtggagcgcctggggcccccgcacagcttgagcccggaaggtctctgggc	911
Db	213	tgggcccccacaaaggtggagcgcctggggcccccgcacagcttgagcccggaaggtctctgggc	154
QY	912	gagcagggcagagtgtaggcgcgcctgcccgcgcacagctctctgggccaactctgacacgttc	971
Db	153	GAGCAGGGGAGGTGACGAGCGCGCTCCCGCCGACGCTCCTGGGCCAACCTGCACCGCTTC	94
QY	972	taggtgcagatgagctgctcctcgagctctctgtctgtctacgtatgcacatgacatctctgccc	1031
Db	93	TAGTGCGCGATGGCTGCGCTCCGCGCTCTGTGCTTACGTATGCATGCATGCCTCGGCC	34
QY	1032	gcggagccacacataaacccttgagcag	1058
Db	33	GGGGAGCCACATATAAACCTTGCGAG	7
RESULT	4		
LOCUS	A1738634/C	844 bp	linear
DEFINITION	willd02.x1 NCI CGAP Col6 Homo sapiens CDNA clone IMAGE:2389923 3'		EST 20-DEC-1999
VERSION	A1738634		
KEYWORDS	MEM22.t3 MSRI repetitive element ;, mRNA sequence.		
SOURCE	A1738634.1 GI:5100615		
ORGANISM	human.		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 844)		
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgsbbs-remail.nih.gov		
	Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.		
	, Ph.D.		
	CNA Library Preparation: M. Bento Soares, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	Clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LNL at:		
	www.bio.lnl.gov/dbirp/image/image.html		
	Insert Length: 1075 Std Error: 0.00		
	Seq primer: -40UP from Gibco		
	High quality sequence stop: 452.		
FEATURES	Location/Qualifiers		
source	1..844		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2389923"		
	/clone.lib="NCI CGAP Col6"		
	/tissue.type="Colon tumor, RER+"		
	/lab.host="DH10B"		
	/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a		
	modified polylinker; Site.1: Not I; Site.2: Eco RI;		
	Plasmid DNA from the normalized library NCI CGAP Col6 was		
	prepared, and ss circles were made in vitro. Following NRP		
	purification, this DNA was used as tracer in a subtractive		
	hybridization reaction. The driver was PCR-amplified cDNAs		
	from a pool of 5 000 clones made from the same library		
	(clonoids 1057416-1061255, and 1144584-1145511).		
	Subtraction by Bento Soares and M. Fatima Bonaldo.		
BASE COUNT	139 a 245 c 302 g 154 t 4 others		
ORIGIN			

Query Match 24.2%; Score 256; DB 9; Length 844;
 Best Local Similarity 99.1%; Pred. No. 8,1e-110;
 Matches 576; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

478 tcagccggccagcaatagctcgaagcaatctgtgagagagagagagagagagagagc 537
 |||||||
 580 tcgacggccggccagcaatagctcgaagcaatctgtgagagagagagagagagagagc 521
 |||||||
 538 agccccaagc 597
 |||||||
 520 accccagc 461
 |||||||
 598 gacccaagc 657
 |||||||
 460 gccccaagc 401
 |||||||
 658 tgcgccaatcctgagagagagagagagagagagagagagagagagagagagc 717
 |||||||
 400 ttgcccgcctctgagagagagagagagagagagagagagagagagagagagc 341
 |||||||
 718 tggccctgacctgctcgcgagagagagagagagagagagagagagagagagc 777
 |||||||
 340 tgcgcccctgacctgctcgcgagagagagagagagagagagagagagagagc 281
 |||||||
 778 gggagc 837
 |||||||
 280 gggagc 221
 |||||||
 838 ccaagc 897
 |||||||
 220 ccaagc 162
 |||||||
 898 agggctgctgagagagagagagagagagagagagagagagagagagagc 957
 |||||||
 161 agggctgctgagagagagagagagagagagagagagagagagagagagc 102
 |||||||
 958 agctgagc 1017
 |||||||
 101 actctgacagc 42
 |||||||
 1018 atactctcctgagagagagagagagagagagagagagagagagagagagc 1058
 |||||||
 41 atactctcctgagagagagagagagagagagagagagagagagagagagc 1

RESULT 5
 AA306055 393 bp mRNA linear EST 18-APR-1997
 LOCUS EST177040 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to
 DEFINITION similar to OX40 homolog, mRNA sequence.
 ACCESSION AA306055
 VERSION AA306055.1 GI:1958383
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 393)
 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulmer, R.A., Bult
 C.J., Lee, N.H., Kinkness, E.F., Weinstock, K.G., Gocayne, J.D., White
 O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,
 Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald,
 L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghegan, N.S., Glodak, A.,
 Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,
 Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Peligri, S.M.,
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shiley, R.,
 Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,
 Benharik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
 Dinke, D., Feng, D.-F., Ferlie, A., Fischer, C., Hastings, G.A., He, M.W.,
 Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,
 Kunsch, C., Hungjun, J., Li, H., Weisner, P.S., Olsen, H., Raymond, L.,
 Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon

JOURNAL
 MEDLINE
 COMMENT
 Bioinformatics
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850 USA
 Fax: 3018699423
 Email: arkerlav@tigr.org
 For clone availability, additional sequence and expression
 information related to this EST, please check the TIGR Human Gene
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)
 Seq primer: M3 Reverse

FEATURES
 source
 1..393
 /organism="Homo sapiens"
 /db_xref="ATCC (Inhost):160207"
 /db_xref="taxon:9606"
 /clone_lib="Jurkat T-cells VI"
 /cell_type="T-lymphocyte"
 /note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
 XhoI"

BASE COUNT 73 a 151 c 124 g 45 t
 ORIGIN

Query Match 22.7%; Score 240; DB 9; Length 393;
 Best Local Similarity 99.7%; Pred. No. 2.7e-102;
 Matches 290; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

281 cagaagtggagc 340
 |||||||
 103 cagaaagtgagc 162
 |||||||
 341 ccgagcggagc 400
 |||||||
 163 ccggcgggagc 222
 |||||||
 401 tccagc 460
 |||||||
 223 tccagc 282
 |||||||
 461 ggcctggagc 520
 |||||||
 283 ggcctggagc 342
 |||||||
 521 ggaacccagc 571
 |||||||
 343 ggaacccagc 393
 |||||||

RESULT 6
 AM293499 471 bp mRNA linear EST 16-JAN-2000
 LOCUS AM293499/C
 DEFINITION UI-H-B12-bhg-a-02-0-UI.s1 NCI-CGAP_Sub4 Homo sapiens cDNA clone
 IMAGE:2727458 3', mRNA sequence.
 ACCESSION AM293499
 VERSION AM293499.1 GI:6700135
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 471)
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 Unpublished (1997)
 Contact: Robert Strausberg, Ph.D.

	Query Match	19.6%	Score 207	DB 9	Length 353
	Best Local Similarity	100.0%	Prod. No. 9,4e-87		
	Matches 207	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	852	ttgggcccaccaaagtgtgacgcttgggcccccgcacgaagcttgagcccgagaggtctgtctgggc	911		
Db	242	tgggcccacaaagctgagcgctggggcccccgcacgcttgagcccgagaggtctgtctgggc	183		
QY	912	gaacgaaggaaggttcgacgagcgccttgcgcgcacgaagctctctgggccaactctgcacgcttc	971		
Db	182	gagcagggcagctgacgagcgcgccttccttcgtactgatatgcataacatcctctggcccc	1031		
QY	972	taagttgcgcgaatgcgctctgcctcgcgctctctgtactgatatgcataacatcctctggcccc	1031		
Db	122	tagctgcccgaatgcgctctgcctcgcgctctctgtactgatatgcataacatcctctggcccc	63		

FEATURES	source
LOCUS	B1833441
DEFINITION	B1833441 743 bp mRNA linear EST 04-OCT-2001 6030880595F1 NIH_MGC_120 Homo sapiens cDNA clone IMAGE:5227199 5', mRNA sequence.
ACCESSION	B1833441
VERSION	B1833441.1 GI:15944991
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 743) NIH-MGC http://mgc.nci.nih.gov/ . National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov
AUTHORS	Tissue Procurement: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Data distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov
COMMENT	Plate: L14M11571 row: m column: 24 High quality sequence stop: 659. location/Qualifiers
	1..743
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone="IMAGE:5227199"
	/clone_1lb="NIH_MGC_120"
	/lab_host="DH10B"
	/note="Organ: pooled pancreas and spleen; Vector:

	Query Match	100.0%	Best Local Similarity	19.2%	Score 203	DB 10	Length 743
	Matches	203	Conservative	0	Mismatches	0	Indels
							Gaps
QY	555	ggccccccgagccagagccatcaactgltccagcccaatgaagcctgtgcccagaactccag	614				
Db	201	ggccccccgagccagagccatcaactgltccagcccaatgaagcctgtgcccagaactccag	260				
QY	615	ggaacctcacccgagcccgatgaggtlcccccgggggcccgtgaggttgcacccaacctctgagc	674				
Db	261	ggacctctcacccgagcccgatgaggtlcccccgggggcccgtgaggttgcacccaacctctgagc	320				
QY	675	ctggagcctggtgctgtgggctgctgtgggcccctgtgacccctgtgacccctgtgacccctgtgac	734				
Db	321	ctggagcctggtgctgtgggctgctgtgggcccctgtgacccctgtgacccctgtgacccctgtgac	380				
QY	735	cgagagagacagagagctgcccc	757				
Db	381	cgagagagacagagagctgcccc	403				

RESULT	9
LOCUS	AM591834/c
DEFINITION	AM591834 198 bp mRNA linear EST 22-MAR-2000
ACCESSION	xx86b03.x1 NCI-CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2850509 3'
VERSION	AM591834
KEYWORDS	AM591834.1 GI:7279000 .
SOURCE	EST .
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryotic Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
JOURNAL	1 (bases 1 to 198)
COMMENT	NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap .
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
	Tumor Gene Index
	Unpublished (1997)
	Contact: Robert Strusberg, Ph.D.
	Email: cgapbs-r@mail.nih.gov
	Life Technologies catalog #: 11547-015
	DNA sequencing by: Washington University Genome Sequencing Center
	Clone distribution: NCI-CGAP clone distribution information can be
	found through the I.M.A.G.E. Consortium/ILM at:
	image.llnl.gov/image/html/resources.shtml
	Seq primer: -400P from Gibco
	High quality sequence stop: 197.
FEATURES	Location/Qualifiers
source	1..198
	/organism="Homo sapiens"
	/db_xref="taxon:9606"
	/clone_image="IMAGE:2850509"
	/clone_id="NCI-CGAP_Lym12"
	/tissue_type="lymphoma, follicular mixed small and large
	cell"
	/lab_host="DH10B"
	/note="Organ: lymph node; Vector: pCMV-SPORT6; Site:1:
	Sal1; Site:2: NotI; Cloned unidirectionally. Primer:
	0180 dT. Average insert size 1.25 kb. Life Technologies
	catalog #: 11547-015"
BASE COUNT	34 a 63 c 69 g 31 t 1 others

```

ORIGIN
Query Match      16.2%; Score 171; DB 9; Length 198;
Best Local Similarity 100.0%; Pred. No. 8.4e-70;
Matches 171; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 888 tggagccggagggtctctgtggcgagcaggtcagagcgctgccccgcacgc 947
      |||||||
Db 177 TGGAGCCCGGAGGCTCTCGGCGAGCGAGGTCCAGGCCGCCCTGCCCGCCAGCGC 118

Qy 948 tccggggcaactctgcacgctttagtgccgatgctctccgggtctgtctag 1007
      |||||||
Db 117 TCCTGGGCGCACTCTGCACCGCTCTAGGTGCCGATGCTGCTCCGCTCTCTGTACG 58

Qy 1008 tatgcatactacctctgcctgcggcgagcacataaaacctgtgcag 1058
      |||||||
Db 57 TATGCAATGACATACCTCTCTGCCCGCGGAGCACAAATAAAACCTTGGCAG 7

RESULT 10
Bi824093      172 bp      mRNA      linear      EST 04-OCT-2001
LOCUS      603039230P1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5180287 5',
DEFINITION      mRNA sequence.
ACCESSION      BI824093
VERSION      BI824093.1 GI:15935643
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 172)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgabbs-remail.nih.gov
      Tissue Procurement: Life Technologies, Inc.
      cDNA Library Preparation: Life Technologies, Inc.
      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.llnl.gov
      Plate: LLM1149 row: k column: 08
      High quality sequence start: 2
      High quality sequence stop: 172.
      Location/Qualifiers
        source
          1..172
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:5180287"
            /clone_11b="NIH_MGC_115"
            /lab_host="DH10B"
            /note="Organ: pooled brain, lung, testis; Vector:
            pCMV-Sport6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
            source anonymous pool of 6 male brains, age range 23-27; 1
            male lung, age 27; and 1 male testis, age 69. Library is
            oligo-dT primed and directionally cloned (EcoRV site is
            destroyed upon cloning). Average insert size 1.8 kb,
            insert size range 1-3 kb. Library is normalized and
            enriched for full-length clones and was constructed by C.
            Gruber (Invitrogen). Research Genetics tracking code
            021. Note: this is a NIH_MGC Library."
BASE COUNT      24 a      54 c      68 g      26 t
ORIGIN
Query Match      13.4%; Score 142; DB 10; Length 172;
Best Local Similarity 100.0%; Pred. No. 3.8e-56;
Matches 142; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 39 ggcggggcgctgtgtgctctctctctgtggcgctgggctgagcagtgagcg 98
      |||||||
Db 31 GGCCTGGGGCGCTGTGCGCGCTCTCTCTCTGGGCGTGGAGCAGCTGACGGGG 90

Qy 99 ctccactgttcgggagacacaccagcagcagctgtctgcacagtgacagcca 158
      |||||||
Db 91 CTCACACTGTCTGGGAGACACTACCCAGACAGACCGGTCTGCCAGAGTGCAGGCCA 150

Qy 159 ggcacgggagtgtgagccgct 180
      |||||||
Db 151 GGCAACGGGAGTGTAGCCGCT 172

RESULT 11
Bi911081      893 bp      mRNA      linear      EST 16-OCT-2001
LOCUS      603069733P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218473 5',
DEFINITION      mRNA sequence.
ACCESSION      Bi911081
VERSION      Bi911081.1 GI:16174620
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE      1 (bases 1 to 893)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
      Email: cgabbs-remail.nih.gov
      Tissue Procurement: Life Technologies, Inc.
      cDNA Library Preparation: Life Technologies, Inc.
      cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
      DNA Sequencing by: Incyte Genomics, Inc.
      Clone distribution: MGC clone distribution information can be
      found through the I.M.A.G.E. Consortium/LNL at:
      http://image.llnl.gov
      Plate: LLM11549 row: b column: 10
      High quality sequence start: 23
      High quality sequence stop: 593.
      Location/Qualifiers
        source
          1..893
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="IMAGE:5218473"
            /clone_11b="NIH_MGC_118"
            /tissue.type="leukocyte"
            /lab_host="DH10B"
            /note="Vector: pCMV-Sport6; Site_1: NotI; Site_2: EcoRV
            (destroyed); RNA source leukocytes from anonymous pool of
            non-activated adult donors. Library is oligo-dT primed
            and directionally cloned (EcoRV site is destroyed upon
            cloning). Average insert size 1.7 kb, insert size range
            1.2-3.3 kb. Library is normalized and enriched for
            full-length clones and was constructed by C. Gruber
            (Invitrogen). Research Genetics tracking code 027. Note:
            this is a NIH_MGC Library."
BASE COUNT      171 a      300 c      272 g      150 t
ORIGIN
Query Match      10.4%; Score 110; DB 10; Length 893;
Best Local Similarity 100.0%; Pred. No. 5.3e-41;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 254 gtgcagccctcagctgtgttaacctcgaagtgagtgagcggaacacactgtgcac 313
      |||||||
Db 231 GTGCAGCCCTCAGCTGTGTAACTCAGAAGTGGAGTGAGCGGAACCACTGTGCAC 290

Qy 314 ggcacacagacacagctgtccgctgcggcgagcgagccagcccttg 363
      |||||||
Db 291 GGCAACAGAGAGACAGTCTGCCGCTGCCGGGGGAGCACCAACGCTCTGG 340

```

```
RESULT 12
LOCUS A1452801/C
DEFINITION t350f10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2144971.3' similar to contains MER22.t3 MER22 repetitive
element ;, mRNA sequence.
ACCESSION A1452801
VERSION A1452801.1 GI:4287894
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 347)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1030 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 323.
FEATURES
source
1..347
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2144971"
/clone_11b="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and as circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HR8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 51 a 100 c 117 g 78 t 1 others
ORIGIN
Query Match 8.9%; Score 94; DB 9; Length 347;
Best Local Similarity 100.0%; Pred. No. 1,7e-33;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 751 tgcgcccgatgccacaagccccctggggagggcagttccggaccccccatccaaggg 810
|||||
DB 331 tgcgcccgatgccacaagccccctggggagggcagttccggaccccccatccaaggg 272
|||||
QY 811 agcaggccgagccgacccatccacccctggccaagat 844
|||||
DB 271 agcaggccgagccgacccatccacccctggccaagat 238
|||||
RESULT 13
LOCUS B1821828
DEFINITION 603035715f1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176899 5',
mRNA sequence.
ACCESSION B1821828
```

```
VERSION B1821828.1 GI:15933378
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 92)
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11440 row: n column: 04
High quality sequence stop: 92.
FEATURES
source
1..92
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5176899"
/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site_1: NotI; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH-MGC Library."
BASE COUNT 17 a 30 c 33 g 12 t
ORIGIN
Query Match 8.7%; Score 92; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.3e-33;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 89 cgtgacggggtccctactgtctgctgggagacactaccacgacgagccggtgtgcacga 148
|||||
DB 1 cgtgacggggtccctactgtctgctgggagacactaccacgacgagccggtgtgcacga 60
|||||
QY 149 gtgcaggccagggacagggatgtgagccgct 180
|||||
DB 61 gtgcaggccagggacagggatgtgagccgct 92
|||||
RESULT 14
LOCUS AA970291/C
DEFINITION op09h05.s1 NCI_CGAP_K16 Homo sapiens cDNA clone IMAGE:1575225 3'
similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ;, mRNA
sequence.
ACCESSION AA970291
VERSION AA970291.1 GI:3145804
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 398)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
```

COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: Stratagene, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.llnl.gov/dbp/image/image.html
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 180.

FEATURES
source
Location/Qualifiers
1. .398
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1575225"
/clone_lib="NCI-CGAP_K1d6"
/sex="mixed"
/tissue_type="kidney tumor"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: kidney; Vector: Bluescript SK-; Site: 1; EcoRI, Site 2; XhoI; Cloned unidirectionally. Primer: Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5' GAATTCGGCAGAG 3' adaptor sequence: 5' CTCGAGTCTTTTCTTTT 3' Average insert size: 1.0 kb."

BASE COUNT 61 a 125 c 146 g 66 t

ORIGIN

Query Match 7.8%; Score 82; DB 9; Length 386;
Best Local Similarity 100.0%; Pred. No. 7.8e-28;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 857 ccaccaggtgagcgtgagcccccagctgagagcccgagagctgcgcggcgagca 916
|||||
Db 189 CCACCAAGTGGACGCTGGGCCCGCCGAGCTGCAGCCGAGGCTGCTGGCGGACGA 130
|||||

Qy 917 gggcaggtgcagagccgctgcc 938
|||||
Db 129 GGGCAGTGCAGCGCCCTGCC 108
|||||

RESULT 15
AI914208 247 bp mRNA linear EST 17-DEC-1999
LOCUS wd76e10.x1 NCI-CGAP_Lu24 Homo sapiens CDNA clone IMAGE:2337546 3',
DEFINITION mRNA sequence.
ACCESSION AI914208
VERSION AI914208.1 GI:5634063
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 247)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: www-bio.llnl.gov/dbp/image/image.html
Insert length: 373 Std Error: 0.00
Seq primer: -40UP from Gibco.
Location/Qualifiers

FEATURES

source
1. .247
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2337546"
/clone_lib="NCI-CGAP_Lu24"
/tissue_type="carcinoid"
/lab_host="DH10B"
/note="Organ: Lung; Vector: pRT73D-Pac (Pharmacia) with a modified polylinker. Plasmid DNA from the normalized library NCI-CGAP_Lu5 was prepared, and ss circles were made in vitro. Following Hsp purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneds 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 41 a 70 c 79 g 57 t

ORIGIN

Query Match 5.5%; Score 58; DB 9; Length 247;
Best Local Similarity 99.1%; Pred. No. 1.5e-16;
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 852 tgggcccaaggtgagcgtgagcccccagctgagagcccgagagctgctgggc 911
|||||
Db 227 TGGGCCCAAGTGGACGCTGGGCCCGCCGAGCTGCAGCCGAGGCTTGTGGGSC 168
|||||

Qy 912 gaggcagaggtgcagagccgctgccgagcagctcctggccaact 960
|||||
Db 167 GAGCAGGCGAGGTGCAGCGCCCTGCCCGCCAGCGCTCTGGGCCACT 119
|||||

RESULT 16
AI91307 668 bp mRNA linear EST 09-MAR-2000
LOCUS w142d05.x1 Soares_Dieckgraefe.colon.NHCD Homo sapiens CDNA clone
DEFINITION IMAGE:2522697 3' similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR
PRECUSOR ;, mRNA sequence.
ACCESSION AI91307
VERSION AI91307.1 GI:5838212
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 668)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
Tumor Gene Index
Unpublished (1997)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-remail.nih.gov
This clone is available royalty-free through ILNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 797 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 217.

FEATURES
source
1. .668
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2522697"
/clone_lib="Soares_Dieckgraefe.colon.NHCD"
/tissue_type="colonic mucosa from 3 patients with Crohn's disease"
/lab_host="DH10B (phage-resistant)"
/note="Organ: colon; Vector: pRT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5' TGTTACCATCTGAGTGGAGGCGGCCCGCTCTTTTCTTTTCTTTT 3'), double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I

the Not I and Eco RI sites of the modified pT7T3 vector.
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library
constructed and normalized by Bento Soares and M. Fatima
Bonaldo."

BASE COUNT 144 a 196 c 152 g 138 t

ORIGIN

Query Match 2.3%; Score 24; DB 9; Length 630;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ccaggcctgcgaagccctggaccac 451
|||||
Db 233 CCAGGCTGCAAGCCCTGGACCAA 256

RESULT 19
AM889471/c 342 bp mRNA linear EST 24-MAY-2000
LOCUS
DEFINITION RC6-NT0029-280400-012-B08 NT0029 Homo sapiens CDNA, mRNA sequence.
AM889471
VERSION AM889471.1 GI:8053676
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 342)
AUTHORS Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H.,
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
Simpson, A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=6t2-RC6-NT0029-280400-012-B08<3-2000-04-28<4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 342.

FEATURES
Source
Location/Qualifiers
1..342
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NT0029"
/dev_stage="Adult"

/note="Organ: nervous_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORSTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the puc 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 83 a 98 c 105 g 56 t

ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 342;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgtggcccttg 708
|||||
Db 72 TGGGCTGCTGGCCCCCTGG 52

RESULT 20
A1823620/c 477 bp mRNA linear EST 21-DEC-1999
LOCUS
DEFINITION w171d07.x1 NCI_CGAP_Kid12 Homo sapiens CDNA clone IMAGE:2398765 3',
mRNA sequence.
A1823620
ACCESSION A1823620.1 GI:5444291
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 477)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bts-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILMIL at:
www-bio.lnlnl.gov/bbrp/image/image.html
Insert length: 811 Std Error: 0.00
Seq primer: 400P from Gibco
High quality sequence stop: 437.

FEATURES
Source
Location/Qualifiers
1..477
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2398765"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1323912-1325831, 1471368-1472903 and
1492104-1493255). Subtraction by Bento Soares and M.
Fatima Bonaldo."

BASE COUNT 104 a 94 c 180 g 97 t 2 others

ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 477;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgtggcccttg 708
|||||
Db 475 TGGGCTGCTGGCCCCCTGG 455

RESULT 21
AA312871 480 bp mRNA linear EST 19-APR-1997
LOCUS
DEFINITION EST183529 Jurkat T-cells VI Homo sapiens CDNA 5' end, mRNA
sequence.
ACCESSION AA312871

VERSION AA312871.1 GI:1965219
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 480)
Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A., Bult
,C.J., Lee,N.H., Kinkness,E.F., Weinstock,K.G., Gocayne,J.D., White
,O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Clayton,R.A.,
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald
,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodke,A.
Gnelm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauder,D.M., Shirley,R.,
Small,K.V., Spriggs,T.A., Uteback,T.R., Weidman,J.F., Li,Y.,
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,
Dinke,D., Feng,D.-F., Ferlie,A., Fischer,C., Hastings,G.A., He,W.M.,
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,
Kunsch,C., Hungjun,D., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon
,M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and
Venter,J.C.
Initial assessment of human gene diversity and expression patterns
based upon 83 million nucleotides of cDNA sequence
Nature 377 (6547 Suppl), 3-174 (1995)
JOURNAL 96026280
MEDLINE Other_ESTs; THC176037
COMMENT Contact: Kerlavage, AR
Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
Tel: 3018699056
Fax: 3018699423
Email: arkerl@vlgf.org
For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (<http://www.tigr.org/cdb/hgi/hgi.html>)
Seq primer: M13 Reverse.
Location/Qualifiers
FEATURES
source 1..480
/organism="Homo sapiens"
/db_xref="ATCC (Inhost):160191"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
/note="Vector: pBluescript SK-; site_1: EcoRI; site_2:
XhoI"

BASE COUNT 75 a 164 c 119 g 117 t 5 others
ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 480;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgctggggcccccctgg 708
|||||
DB 237 tggggctgctggggcccccctgg 257

RESULT 22
A1126122/c 482 bp mRNA linear EST 28-OCT-1998
LOCUS A1126122
DEFINITION gq77b04.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1735471
3', mRNA sequence.
ACCESSION A1126122
VERSION A1126122.1 GI:3594636
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 482)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo
, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution Information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
Insert Length: 723 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amerham
High quality sequence stop: 444.
Location/Qualifiers
FEATURES
source 1..482
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:1735471"
/clone_lib="Soares_testis_NHT"
/sex="male"
/lab_host="DH10B"
/note="Vector: p77T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
was prepared from mRNA obtained from Clontech Laboratories
, Inc., and primed with a Not I - oligo(dT) primer [5'
TGTTCACATCGTAGTGAGCGCGCGCCCAATTTTCTTTT 3']
Double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not I
and Eco RI sites of the modified p77T3 vector. Library
went through one round of normalization to Cot5, and was
constructed by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 107 a 98 c 183 g 93 t 1 others
ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 482;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgctggggcccccctgg 708
|||||
DB 471 tggggctgctggggcccccctgg 451

RESULT 23
AA477725/c 545 bp mRNA linear EST 09-NOV-1997
LOCUS AA477725
DEFINITION zu44f11.s1 Soares ovary tumor Nshot Homo sapiens cDNA clone
IMAGE:740877 3', mRNA sequence.
ACCESSION AA477725
VERSION AA477725.1 GI:2206359
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 545)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Getsef,G., Jost,S.,
Kizman,D., Kucada,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
JOURNAL Contact: Wilson RK
COMMENT Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810

Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 688 tggggctgctggggccctcg 708
|||||
Db 178 TGGGCTGCTGGGCCCTGG 198

RESULT 26
AI264358 636 bp mRNA linear EST 27-JAN-1999
LOCUS q109f04.x1 Soares.NHMPu.S1 Homo sapiens cDNA clone IMAGE:1855999
DEFINITION 3' similar to TR:O42154 O42154 GLUCOSE-6-PHOSPHATASE ;, mRNA
sequence.

ACCESSION AI264358
VERSION AI264358.1 GI:3872561
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 636)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Insert length: 720 Std Error: 0.00
Seq primer: -40up from G1bco
High quality sequence stop: 399.
Location/Qualifiers
1. 636
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1855999"
/clone_1lb="Soares.NHMPu.S1"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site: 1: Not I;
Site: 2: Eco RI. Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2bDHu, pregnant uterus
NbDHu, and fetal heart NbH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

BASE COUNT 138 a 150 c 228 g 116 t 4 others
ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 636;
Best Local Similarity 100.0%; Pred. No. 45;
Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 688 tggggctgctggggccctcg 708
|||||
Db 461 TGGGCTGCTGGGCCCTGG 441

RESULT 27
AI669655 649 bp mRNA linear EST 17-DEC-1999
LOCUS wc12a05.x1 NCI-CGAP_Pr28 Homo sapiens cDNA clone IMAGE:2314928 3'
DEFINITION similar to TR:O42154 O42154 GLUCOSE-6-PHOSPHATASE ;, mRNA sequence.
ACCESSION AI669655
VERSION AI669655.1 GI:4834429
KEYWORDS EST.

SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 649)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
www.bio.lnl.gov/bdhp/image/image.html
Insert length: 768 Std Error: 0.00
Seq primer: -40up from G1bco
High quality sequence stop: 454.
Location/Qualifiers
1. 649
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2314928"
/clone_1lb="NCI-CGAP_Pr28"
/sex="male"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; Plasmid DNA from the
normalized library NCI-CGAP_Pr22 was prepared, and ss
circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
985608-986759, 1101192-1101959, and 1217928-1220615).
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 141 a 154 c 230 g 117 t 7 others
ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 649;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 688 tggggctgctggggccctcg 708
|||||
Db 468 TGGGCTGCTGGGCCCTGG 448

RESULT 28
BM006189 650 bp mRNA linear EST 30-OCT-2001
LOCUS 603614011P1 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:5433602 5',
DEFINITION mRNA sequence.
ACCESSION BM006189
VERSION BM006189.1 GI:16520543
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 650)
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM1909 row: f column: 03
 High quality sequence stop: 650.

FEATURES

source

1. .650
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="5433602"
 /clone_lib="NIH_MGC_100"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: liver; Vector: pORF7; Site.1: XhoI; Site.2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-CDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

BASE COUNT 128 a 234 c 149 g 139 t

ORIGIN

Query Match 2.0%; Score 21; DB 10; Length 650;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgctggggcccttg 708
 |||
 Db 162 TGGGGCTGCTGGGGCCCTCG 182

RESULT 29

BF725110 653 bp mRNA linear EST 05-JAN-2001
 LOCUS
 DEFINITION bx12c11.y1 Human Iris cDNA (un-normalized, unamplified): Bx Homo
 sapiens CDNA clone bx12c11 5', mRNA sequence.

ACCESSION BF725110
 VERSION BF725110.1 GI:12041021
 KEYWORDS
 SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 653)

REFERENCE

AUTHORS Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
 TITLE Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.
 JOURNAL Invest. Ophthalmol. Vis. Sci. 41 (2000) In press

COMMENT

Contact: Wistow G
 Section on Molecular Structure and Function
 National Eye Institute
 6/331, NIH, Bethesda, MD 20892-2740, USA
 Tel: 301 402 3452
 Fax: 301 496 0078
 Email: graeme@helix.nih.gov
 Plate: 12 row: c column: 11
 Seq primer: M13RPI reverse primer (ABI).

FEATURES

source

1. .653
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="bx12c11"
 /clone_lib="Human Iris cDNA (un-normalized, unamplified):
 Bx"
 /tissue_type="Iris"
 /dev_stage="Adult"
 /lab_host="EMDH10B"
 /note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris

tissue was pooled from 10 individuals ranging in age from
 4-80 years and RNA was extracted. From this pooled sample
 an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A
 directionally cloned cDNA library in the pCMVSPORT6 vector
 was constructed at Life Technologies, essentially
 following the protocols of the Superscript Plasmid System
 full details of which are contained in the manufacturer's
 instruction manual (<http://www.lifetech.com/>). First
 strand synthesis was carried out using a Not I
 primer-adaptor [5'-TGACATGTTCTAGATCGGACGGCCGCTT)15-3'
]. Not I/Dint end inserts were cloned into the Not I/EcoR
 V sites in the vector. EST analysis was performed on the
 unamplified library at the NIH Intramural Sequencing
 Center (NISC)."

BASE COUNT 101 a 208 c 183 g 161 t

ORIGIN

Query Match 2.0%; Score 21; DB 10; Length 653;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgctggggcccttg 708
 |||
 Db 553 TGGGGCTGCTGGGGCCCTCG 573

RESULT 30

BG422683 683 bp mRNA linear EST 14-MAR-2001
 LOCUS
 DEFINITION 602449189P1 NIH_MGC_14 Homo sapiens CDNA clone IMAGE:4587551 5',
 mRNA sequence.

ACCESSION BG422683
 VERSION BG422683.1 GI:13329189
 KEYWORDS
 SOURCE

ORGANISM

human.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 683)

REFERENCE

AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov

COMMENT

Tissue Procurement: DCRD/DMP
 CDNA Library Preparation: Ling Hong/Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LNCM1318 row: a column: 24
 High quality sequence stop: 664.

FEATURES

source

1. .683
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="4587551"
 /clone_lib="NIH_MGC_14"
 /tissue_type="renal cell adenocarcinoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: kidney; Vector: pORF7; Site.1: XhoI; Site.2:
 EcoRI; CDNA made by oligo-dT priming. Directionally
 cloned into EcoRI/XhoI sites using the following 5'
 adaptor: GGCACGAG(G). Size-selected >500bp for average
 insert size 1.8kb. Library constructed by Ling Hong in
 the laboratory of Gerald M. Rubin (University of
 California, Berkeley) using ZAP-CDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT

134 a 236 c 161 g 152 t

ORIGIN

Query Match 2.0%; Score 21; DB 10; Length 683;
Best Local Similarity 100.0%; Pred.No. 46;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 688 tgggctgtgtggcccccctgg 708
|||||
DB 199 tgggctgtgtggcccccctgg 219

Search completed: June 19, 2002, 01:45:26
Job time: 2007 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:17:49 ; Search time 202.93 Seconds
(without alignments)
8951.340 Million cell updates/sec

Title: US-09-852-845-1
Perfect score: 1058
Sequence: 1 cagcagagacagagatgtgc.....cacataaaacctgtgcag 1058

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : N_Geneseq_032802.*

1: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT:*
2: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:*
3: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:*
4: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT:*
5: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT:*
6: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:*
7: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT:*
8: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:*
9: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1989.DAT:*
10: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT:*
11: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT:*
12: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1992.DAT:*
13: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1993.DAT:*
14: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1994.DAT:*
15: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT:*
16: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT:*
17: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1997.DAT:*
18: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1998.DAT:*
19: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1999.DAT:*
20: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT:*
21: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:*
22: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:*
23: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*
24: /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	886	83.7	1057	AAQ88758	ACT-4 cell surface
2	886	83.7	1057	AAQ88758	ACT-4 h-1 receptor
3	886	83.7	1057	AAQ88758	Human OX-40 CDNA
4	83	7.8	117	AAH24886	Oligonucleotide fo
5	83	7.8	117	AAH24886	Human secondary si
6	83	7.8	117	AAH24886	Human secondary si
7	78	7.4	117	AAH24887	Oligonucleotide fo
8	78	7.4	117	AAH24887	Human secondary si
9	78	7.4	117	AAH24887	Human secondary si

10	28	2.6	618	16	AAQ0826
11	28	2.6	618	19	AAV32640
12	28	2.6	1317	16	AAQ0829
13	28	2.6	1317	19	AAV32636
14	24	2.3	5148	22	AAQ35255
15	23	2.2	5148	22	AAQ35255
16	22	2.1	22	22	AAH42273
17	21	2.0	22	22	AAH42273
18	21	2.0	1153	21	AAH87680
19	21	2.0	1467	21	AACT6846
20	21	2.0	1467	22	AAK52633
21	21	2.0	1569	22	AAH22958
22	21	2.0	1658	22	AAK51649
23	21	2.0	5808	22	AAH36023
24	21	2.0	5808	22	AAK69724
25	21	2.0	38348	22	AAK84953
26	20	1.9	4466	23	ABL17164
27	20	1.9	6361	23	ABL15756
28	20	1.9	38272	22	AAK84952
29	19	1.8	19	22	AAH22274
30	19	1.8	637	22	AAK87821
31	19	1.8	883	22	AAH23724
32	19	1.8	884	21	AAZ51624
33	19	1.8	1110	22	ABA20758
34	19	1.8	1210	22	AAH23725
35	19	1.8	1356	21	AACT6656
36	19	1.8	1389	19	AAV29992
37	19	1.8	1413	20	AAK59084
38	19	1.8	1516	22	AAV28357
39	19	1.8	1622	17	AACT34592
40	19	1.8	1981	21	AAZ98207
41	19	1.8	2713	22	AAH23726
42	19	1.8	3086	22	AAE27649
43	19	1.8	6114	20	AAH23490
44	19	1.8	6132	20	AAH23489
45	19	1.8	7898	20	AAK59080
46	19	1.8	7898	20	AAK59081
47	19	1.8	12286	22	AAK42019
48	19	1.8	12286	22	AAK89560
49	18	1.7	47	21	AAZ69360
50	18	1.7	107	22	ABA50988

ALIGNMENTS

RESULT 1	
AAQ88758	standard; CDNA: 1057 BP.
AAQ88758;	
21-NOV-1995	(first entry)
ACT-4 cell surface receptor CDNA sequence.	
Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system;	
ss.	
Homo sapiens.	
Key	Location/Qualifiers
CDS	15..845
FT	/*tag= a
FT	15..86
FT	/*tag= b
FT	1042..1047
FT	/*tag= c
polyA-site	
W09512673-A.	
11-MAY-1995.	

Mouse type-II memb
Mouse OX40 extrace
Plasid pDC406/OX4
OX40/Fc CDNA. Syn
PCR primer 1 for h
Tumour suppressor
OX40 reverse PCR p
OX40 forward PCR p
Human secreted pro
Human ORF2401
Human polynucleoti
Human phosphatase
Human polynucleoti
Human musculoskele
Human immune/haema
Drosophila melanog
Human immune/haema
OX40 hybridisation
Human digestive sy
Oligonucleotide #3
Human membrane cha
Human nervous syst
Oligonucleotide #4
Human ORF2211
Human BY55 CDNA se
Human activated ca
Human BBSR PLP CDN
NTT-11 nerve prot
Human signal pepti
Oligonucleotide #5
DNA encoding human
Human T-type volta
Human activated ca
Human activated ca
Genomic sequence #
Human histone deac
Human map-related
Human breast cell

CC activated autoantigen-specific CD4+ T-cells present at the site of
 CC inflammation but absent on CD4+ T-cells at non-inflammatory sites)
 CC and CDNA encoding the antigen was isolated. PCR primers were
 CC designed and used to clone murine OX-40 cDNA by PCR from RNA
 CC isolated from murine CD4+ T-cells activated with concanavalin A.
 CC Then the murine OX-40 cDNA was used to probe a cDNA lambda gtl1
 CC library from human activated T lymphocytes to obtain human OX-40
 CC cDNA. The published patent application states that the OX-40 cDNA
 CC sequence is also in SQ ID no. 1, but this sequence is not present
 CC in the spec. A nucleic acid having the sequence in SQ ID no 1 and
 CC the polypeptide encoded by it are claimed.

SO Sequence 834 BP; 144 A; 298 C; 270 G; 122 T; 0 other;

Query Match 26.6%; Score 281; DB 16; Length 834;
 Best Local Similarity 100.0%; Pred. No. 5.6e-116;
 Matches 281; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 atgtcggtggggctcggcgctgggcccggcgctgtgagctctctctcctcggc 74
 DB 1 atgtcggtggggctcggcgctgggcccggcgctgtgagctctctcctcggc 60
 QY 75 ctgggctgagcaccgtgaggggctccactgtgtcggggagaccctaccacagcagac 134
 DB 61 ctgggctgagcaccgtgaggggctccactgtgtcggggagaccctaccacagcagac 120
 QY 135 cgggtgctccacagctgcagggccagggagatgtgtagccgctgcagccgctccag 194
 DB 121 cgggtgctccacagctgcagggccagggagatgtgtagccgctgcagccgctccag 180
 QY 195 aacacggtgtccgctcgtgctggcgccggtcttacaagactgtgtcagctcagcgg 254
 DB 181 aacacggtgtcgtcgtcgtgctggcgccggtcttacaagactgtgtcagctcagcgg 240
 QY 255 tgcagagccctgcagctgtgttaacctcagaagtggagatga 295
 DB 241 tgcagagccctgcagctgtgttaacctcagaagtggagatga 281

RESULT 4
 AAH24886
 ID AAH24886 standard; DNA; 117 BP.

AC AAH24886;

DT 22-AUG-2001 (first entry)

DE Oligonucleotide for a secondary signalling motif.

XX Stimulatory primary signalling motif; immune cell; signal transduction;
 KW chimeric receptor; inflammatory disease; autoimmune disease; asthma;
 KW eczema; congenital disease; cystic fibrosis; sickle cell anemia;
 KW dermatological disease; psoriasis; neurological disease;
 KW multiple sclerosis; transplant-related disease; metabolic disease;
 KW organ transplant rejection; graft versus host disease;
 KW idiopathic disease; diabetes; cancer; ss.

XX Synthetic.

XX WO200132709-A2.

XX 10-MAY-2001.

XX 01-NOV-2000; 2000WO-GB04183.

XX 01-NOV-1999; 99GB-0025848.

XX (CELL-) CELLTech CHIROSCIENCE LTD.

XX Flinney HM, Lawson ADG;

XX 'WPI, 2001-389718/41.

XX Novel cytoplasmic signalling protein and chimeric receptor protein,
 PT useful for treating HIV infection, asthma, eczema, psoriasis, multiple
 PT sclerosis, contain non-natural stimulatory primary signalling motif -
 PS Example 2; Fig 3; 45pp; English.

XX Oligonucleotides AAH24886-87 were used to construct DNA encoding
 CC secondary signalling sequences. The specification describes stimulatory
 CC primary signalling motifs. Primary motifs are efficient at at
 CC mediating immune cell signal transduction, particularly when
 CC incorporated in an intracellular signalling domain of a chimeric
 CC receptor. The primary signalling motif can be combined in any way so
 CC as to achieve the desired level of activation (or inhibition) of a
 CC number of secondary messenger cascades. The signalling motifs are useful
 CC in therapy and in the manufacture of medicament for treating or
 CC preventing disease in humans or animals. They are useful for treating
 CC human patients suffering from infectious diseases e.g. human
 CC immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases
 CC such as asthma and eczema, congenital diseases e.g. cystic fibrosis,
 CC sickle cell anemia, dermatological diseases e.g. psoriasis, neurological
 CC diseases e.g. multiple sclerosis, transplant-related disease e.g. organ
 CC transplant rejection, graft versus host disease, metabolic/idiopathic
 CC disease e.g. diabetes, and cancer.

SO Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;

Query Match 7.8%; Score 83; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 2.3e-27;
 Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 cggagagaccagagagctgcgcccgatgccacaaagcccttggggagagcagttccgg 794
 DB 6 cggagagaccagagagctgcgcccgatgccacaaagcccttggggagagcagttccgg 65
 QY 795 accccatccagagagcagc 817
 DB 66 accccatccagagagcagc 88

RESULT 5
 AAH24477
 ID AAH24477 standard; DNA; 117 BP.

AC AAH24477;

DT 07-AUG-2001 (first entry)

DE Human secondary signalling motif SB34 oligo F1340A.

XX Human; primary signalling motif; sequence block; SB; immunosuppressive;
 KW secondary signalling sequence; antimicrobial; anti-inflammatory;
 KW dermatological; neuroprotective; cytostatic; anti-HIV; antiasthmatic;
 KW antischlicking; antipsoriatic; antidiabetic; gene therapy; diabetes;
 KW immune cell signal transduction; infection; inflammation; cancer;
 KW autoimmune disease; congenital disease; psoriasis; neurological disease;
 KW organ transplant rejection; ss.

XX Homo sapiens.

XX WO200132867-A1.

XX 10-MAY-2001.

XX 01-NOV-2000; 2000WO-GB04193.

XX 01-NOV-1999; 99GB-0025853.

XX (CELL-) CELLTech CHIROSCIENCE LTD.

XX Flinney HM, Lawson ADG;

DR WPI: 2001-328791/34.
XX
XX New nucleic acids encoding polypeptides with expanded primary signalling
PT motifs, for use in gene therapy, particularly for treating or
PT preventing infections, inflammations or autoimmune diseases in humans
XX
XX
PS Example 2: Fig 3; 43pp; English.
XX
CC The invention relates to novel primary signalling motifs containing
CC a consensus amino acid sequence. These motifs are extremely
CC efficient at mediating immune cell signal transduction, particularly
CC when incorporated into an intracellular signalling domain of a chimeric
CC receptor. Nucleic acids that encode, and polypeptides that contain,
CC these primary signalling motifs are useful in medicine and research.
CC They are useful in therapy, or in the manufacture of a medicament for
CC treating or preventing disease in humans or in animals. These diseases
CC include infections (e.g. HIV (human immunodeficiency virus) infection),
CC inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital
CC diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological
CC diseases (e.g. psoriasis), neurological diseases (e.g. multiple
CC sclerosis), organ transplant rejection or graft-versus-host disease, or
CC metabolic/diopathic diseases (e.g. diabetes or cancer). The
CC present sequence is one of a large number of oligonucleotides used in
CC the construction of sequence blocks (SBS) of primary and secondary
CC signalling motifs. Primary signalling motifs are sequences that
CC transduce either a stimulatory or an inhibitory signal, which regulates
CC primary activation of the T cell receptor (TCR) complex. Secondary
CC motifs impart secondary or co-stimulatory signalling capacity to a
CC molecule in T cells.
XX
SQ Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;

Query Match 7.8%; Score 83; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 cggagggaccagagctgcccccgatgccacaagccccctggggagagcagtttcgg 794
Db 6 cggagggaccagagctgcccccgatgccacaagccccctggggagagcagtttcgg 65
|||||
QY 795 accccatccaagagagcagc 817
Db 66 accccatccaagagagcagc 88
|||||

RESULT 6
AAH24543
ID AAH24543 standard; DNA; 117 BP.
XX
XX
AC AAH24543;
XX
DT 08-AUG-2001 (first entry)
XX
DE Human secondary signalling motif SB34 oligo F1340A.
XX
XX Human: anti-HIV; antiinflammatory; antiasthmatic; dermatological;
KW antisickling; antipsoriatic; neuroprotective; immunosuppressive;
KW antidiabetic; cytostatic; HIV infection; inflammation;
KW autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;
KW neurological disease; organ transplant rejection; diabetes; cancer;
KW graft-versus-host disease; adaptor receptor protein; sequence block;
KW SB; primary signalling motif; secondary signalling motif; ss.
XX
XX
OS Homo sapiens.
XX
PN WO200132866-A2.
XX
PD 10-MAY-2001.
XX
PF 01-NOV-2000; 2000WO-GB04189.
XX

PR 01-NOV-1999; 99GB-0025854.
XX
XX
PA (CELL-) CELLTECH CHIROSCIENCE LTD.
XX
XX
P1 Finney HM, Lawson ADG;
XX
XX
DR WPI: 2001-328790/34.
XX
XX
PT Novel polynucleotide encoding adaptor receptor protein useful for
PT treating human immunodeficiency virus (HIV) infection, asthma, cystic
PT fibrosis, multiple sclerosis, organ transplant rejection, diabetes and
PT cancer
XX
XX
PS Example 3: Fig 3; 52pp; English.
XX
CC The invention relates to a novel nucleic acid encoding an adaptor
CC receptor protein comprising an extracellular ligand-binding domain, a
CC transmembrane domain and an intracellular signalling domain. The
CC intracellular signalling domain comprises the cytoplasmic portion of at
CC least one adaptor protein, and the extracellular ligand-binding domain
CC is not CD8 or a major histocompatibility complex (MHC) class I protein.
CC The adaptor receptor protein and the nucleic acid encoding it are useful
CC in therapy. They are useful in the manufacture of a medicament for the
CC treatment or prevention of disease in humans and animals. They are useful
CC in the treatment of infectious diseases (e.g. HIV infection),
CC inflammatory and autoimmune diseases (e.g. asthma and eczema),
CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia),
CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g.)
CC multiple sclerosis), organ transplant rejection, graft-versus-host
CC disease and metabolic/diopathic diseases such as diabetes and cancer.
CC The present sequence is one of a large number of oligonucleotides used
CC in the construction of sequence blocks (SBS) of primary and secondary
CC signalling motifs. Primary signalling motifs transduce either a
CC stimulatory or an inhibitory signal, which regulates primary activation
CC of the T cell receptor (TCR) complex. Secondary signalling motifs impart
CC secondary or co-stimulatory signalling capacity to a molecule in T
CC cells. Primary and secondary signalling motifs may be used as
CC components of the adaptor receptor protein of the invention.
XX
SQ Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;

Query Match 7.8%; Score 83; DB 22; Length 117;
Best Local Similarity 100.0%; Pred. No. 2.3e-27;
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 735 cggagggaccagagctgcccccgatgccacaagccccctggggagagcagtttcgg 794
Db 6 cggagggaccagagctgcccccgatgccacaagccccctggggagagcagtttcgg 65
|||||
QY 795 accccatccaagagagcagc 817
Db 66 accccatccaagagagcagc 88
|||||

RESULT 7
AAH24887/C
ID AAH24887 standard; DNA; 117 BP.
XX
XX
AC AAH24887;
XX
DT 22-AUG-2001 (first entry)
XX
DE Oligonucleotide for a secondary signalling motif.
XX
XX Stimulatory primary signalling motif; immune cell; signal transduction;
KW chimeric receptor; inflammatory disease; autoimmune disease; asthma;
KW eczema; congenital disease; cystic fibrosis; sickle cell anaemia;
KW dermatological disease; psoriasis; neurological disease;
KW multiple sclerosis; transplant-related disease; metabolic disease;
KW organ transplant rejection; graft versus host disease;
KW idiopathic disease; diabetes; cancer; ss.
XX

```
OS Synthetic.
XX WO200132709-A2.
XX 10-MAY-2001.
XX 01-NOV-2000; 2000WO-GB04183.
XX 01-NOV-1999; 99GB-0025848.
XX (CELL-) CELLTech CHIROSCIENCE LTD.
XX Finney HM, Lawson ADG;
XX WPI; 2001-389718/41.
XX
XX Novel cytoplasmic signalling protein and chimeric receptor protein,
XX useful for treating HIV infection, asthma, eczema, psoriasis, multiple
XX sclerosis, contain non-natural stimulatory primary signalling motif -
XX
XX Example 2; Fig 3; 45pp; English.
XX
XX Oligonucleotides AAH24886-87 were used to construct DNA encoding
XX secondary signalling sequences. The specification describes stimulatory
XX primary signalling motifs. Primary motifs are efficient at at
XX mediating immune cell signal transduction, particularly when
XX incorporated in an intracellular signalling domain of a chimeric
XX receptor. The primary signalling motif can be combined in any way so
XX as to achieve the desired level of activation (or inhibition) of a
XX number of secondary messenger cascades. The signalling motifs are useful
XX in therapy and in the manufacture of medication for treating or
XX preventing disease in humans or animals. They are are useful for treating
XX human patients suffering from infectious diseases e.g. human
XX immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases
XX such as asthma and eczema, congenital diseases e.g. cystic fibrosis,
XX sickle cell anemia, dermatological diseases e.g. psoriasis, neurological
XX diseases e.g. multiple sclerosis, transplant-related disease e.g. organ
XX transplant rejection, graft versus host disease, metabolic/idiopathic
XX disease e.g. diabetes, and cancer.
XX
XX Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;
XX
XX Query Match 7.4%; Score 78; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 4e-25;
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 768 aagcccccctggggagagcagttccgcgaccccatcacaagagagagcagccgaccac 827
XX |||||||
XX DB 83 AAGCCCCCTGGGGAGAGCAAGTTCCGACCCCATCAAGAGAGAGCGCCGACGCCAC 24
XX
XX QY 828 tccaccctggccaagatc 845
XX |||||||
XX DB 23 TCCACCCCTGGCCAAAGATC 6
XX
XX RESULT 8
XX AAH24478/c
XX ID AAH24478 standard; DNA; 117 BP.
XX
XX AC AAH24478;
XX
XX DT 07-AUG-2001 (first entry)
XX
XX DE Human secondary signalling motif SB34 oligo F1340B.
XX
XX KW Human; primary signalling motif; sequence block; SB; immunosuppressive;
XX secondary signalling sequence; antimicrobial; anti-inflammatory;
XX dermatological; neuroprotective; cytostatic; anti-HIV; antiasthmatic;
XX antisludging; antipsoriatic; antidiabetic; gene therapy; diabetes;
XX immune cell signal transduction; infection; inflammation; cancer;
XX autoimmune disease; congenital disease; psoriasis; neurological disease;
XX organ transplant rejection; ss.
```

```
XX OS Homo sapiens.
XX WO200132867-A1.
XX 10-MAY-2001.
XX 01-NOV-2000; 2000WO-GB04193.
XX 01-NOV-1999; 99GB-0025853.
XX (CELL-) CELLTech CHIROSCIENCE LTD.
XX Finney HM, Lawson ADG;
XX WPI; 2001-328791/34.
XX
XX New nucleic acids encoding polypeptides with expanded primary signalling
XX motifs, for use in gene therapy, particularly for treating or
XX preventing infections, inflammations or autoimmune diseases in humans
XX
XX Example 2; Fig 3; 43pp; English.
XX
XX The invention relates to novel primary signalling motifs containing
XX a consensus amino acid sequence. These motifs are extremely
XX efficient at mediating immune cell signal transduction, particularly
XX when incorporated into an intracellular signalling domain of a chimeric
XX receptor. Nucleic acids that encode, and polypeptides that contain,
XX these primary signalling motifs are useful in medicine and research.
XX They are useful in therapy, or in the manufacture of a medication for
XX treating or preventing disease in humans or in animals. These diseases
XX include infections (e.g. HIV (human immunodeficiency virus) infection),
XX inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital
XX diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological
XX diseases (e.g. psoriasis), neurological diseases (e.g. multiple
XX sclerosis), organ transplant rejection or graft-versus-host disease, or
XX metabolic/idiopathic diseases (e.g. diabetes or cancer). The
XX present sequence is one of a large number of oligonucleotides used in
XX the construction of sequence blocks (SBs) of primary and secondary
XX signalling motifs. Primary signalling motifs are sequences that
XX transduce either a stimulatory or an inhibitory signal, which regulates
XX CC primary activation of the T cell receptor (TCR) complex. Secondary
XX motifs impart secondary or co-stimulatory signalling capacity to a
XX molecule in T cells.
XX
XX Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;
XX
XX Query Match 7.4%; Score 78; DB 22; Length 117;
XX Best Local Similarity 100.0%; Pred. No. 4e-25;
XX Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 768 aagcccccctggggagagcagttccgcgaccccatcacaagagagagcagccgaccac 827
XX |||||||
XX DB 83 AAGCCCCCTGGGGAGAGCAAGTTCCGACCCCATCAAGAGAGAGCGCCGACGCCAC 24
XX
XX QY 828 tccaccctggccaagatc 845
XX |||||||
XX DB 23 TCCACCCCTGGCCAAAGATC 6
XX
XX RESULT 9
XX AAH24544/c
XX ID AAH24544 standard; DNA; 117 BP.
XX
XX AC AAH24544;
XX
XX DT 08-AUG-2001 (first entry)
XX
XX DE Human secondary signalling motif SB34 oligo F1340B.
XX
XX KW Human; anti-HIV; anti-inflammatory; antiasthmatic; dermatological;
```

KW antisickling; antipsoriatic; neuroprotective; immunosuppressive;
 KW antidiabetic; cytostatic; HIV infection; inflammation;
 KW autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;
 KW neurological disease; organ transplant rejection; diabetes; cancer;
 KW graft-versus-host disease; adaptor receptor protein; sequence block;
 KW S8; primary signalling motif; secondary signalling motif; ss.
 XX
 OS Homo sapiens.
 XX
 PN W0200132866-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 01-NOV-2000; 2000WO-GB04189.
 XX
 PR 01-NOV-1999; 99GB-0025854.
 XX
 PA (CELL-) CELLTech CHIROSCIENCE LTD.
 XX
 PI Flinney HM, Lawson ADG;
 XX
 DR WPI; 2001-328790/34.
 XX
 XX Example 3; Fig 3; 52pp; English.
 XX
 CC The invention relates to a novel nucleic acid encoding an adaptor
 CC receptor protein comprising an extracellular ligand-binding domain, a
 CC transmembrane domain and an intracellular signalling domain. The
 CC intracellular signalling domain comprises the cytoplasmic portion of at
 CC least one adaptor protein, and the extracellular ligand-binding domain
 CC is not C88 or a major histocompatibility complex (MHC) class I protein.
 CC The adaptor receptor protein and the nucleic acid encoding it are useful
 CC in therapy. They are useful in the manufacture of a medicament for the
 CC treatment or prevention of disease in humans and animals. They are useful
 CC in the treatment of infectious diseases (e.g. HIV infection),
 CC inflammatory and autoimmune diseases (e.g. asthma and eczema),
 CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia),
 CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g.)
 CC multiple sclerosis), organ transplant rejection, graft-versus-host
 CC disease and metabolic/diopathic diseases such as diabetes and cancer.
 CC The present sequence is one of a large number of oligonucleotides used
 CC in the construction of sequence blocks (Sbs) of primary and secondary
 CC signalling motifs. Primary signalling motifs transduce either a
 CC stimulatory or an inhibitory signal, which regulates primary activation
 CC of the T cell receptor (TCR) complex. Secondary signalling motifs impart
 CC secondary or co-stimulatory signalling capacity to a molecule in T
 CC cells. Primary and secondary signalling motifs may be used as
 CC components of the adaptor receptor protein of the invention.
 XX
 XX Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;
 XX
 XX
 Query Match 7.4%; Score 78; DB 22; Length 117;
 Best Local Similarity 100.0%; Pred. No. 4e-25;
 Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 768 aagcccccctggggagagcatttcgcgaccccccatcacaagagagcagcagccacac 827
 DB 83 AAGCCCCCTGGGGGAGGAGCGATTTCGCGACCCCATCATCAAGAGAGACAGCGCCGCCAC 24
 QY 828 tccacctgcccagaatc 845
 DB 23 TCCACCTGTGCGCAAGATC 6
 RESULT 10
 AAT00826
 ID AAT00826 standard; cDNA to mRNA; 618 BP.

XX
 XX AAT00826;
 AC 30-MAR-1996 (first entry)
 DT
 DE Mouse type-II membrane polypeptide OX40 extracellular domain.
 DE
 XX OX40; OX40-L; cytokine; cell surface molecule;
 KW membrane glycoprotein; ss.
 KW
 OS Mus musculus.
 XX
 PN US5457035-A.
 XX
 PD 10-OCT-1995.
 XX
 PF 23-JUL-1993; 93US-0097827.
 XX
 PR 23-JUL-1993; 93US-0097827.
 XX
 PA (IMV) IMMUNEX CORP.
 XX
 PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
 XX
 DR WPI; 1995-357992/46.
 DR P-PSDB; AAR81881.
 XX
 PT New isolated DNA encoding the OX40 ligand polypeptide - also vectors
 PT and host cells, used to produce recombinant ligand used in e.g.
 PT prim. T cell culture, to modulate immune response etc.
 XX
 PS Example 1; Column 31-32; 26pp; English.
 XX
 CC This sequence encodes the extracellular domain of OX40, a membrane
 CC glycoprotein present on the CD4 positive subset of activated T
 CC cells.
 CC
 CC Sequence 618 BP; 148 A; 187 C; 151 G; 132 T; 0 other;
 SQ
 Query Match 2.6%; Score 28; DB 16; Length 618;
 Best Local Similarity 100.0%; Pred. No. 0.0079;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 424 acaaccagcctgcaagccctggaccac 451
 DB 404 acaaccagcctgcaagccctggaccac 431
 RESULT 11
 AAV32640
 ID AAV32640 standard; cDNA to mRNA; 618 BP.
 AC AAV32640;
 XX
 DT 25-SEP-1998 (first entry)
 DE
 XX Mouse OX40 extracellular domain encoding cDNA.
 DE
 XX OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L;
 KW OX40/Fc; ss.
 KW
 OS Mus sp.
 XX
 FH Key
 FT CDS
 FT
 FT Location/Qualifiers
 FT 1..618
 FT /tag= a
 FT /product= "Mouse OX40 extracellular region"
 FT /note= "CDS does not contain a stop codon"
 XX
 PN US5783665-A.
 XX
 PD 21-JUL-1998.


```
XX 23-JUL-1993; 93US-0097827.
PR 22-JUN-1995; 95US-0494574.
XX (IMMUNEX CORP.
PA Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
XX WPI: 1998-427099/36.
DR P-PSDB: AAM48976.
XX
PT Purified polypeptide OX-40 ligands - for co-stimulation of T-cell
PT production and binding assays for OX-40 and homologues
XX
PS Example 2; Col 35-38; 26pp; English.
XX
CC The present sequence represents the OX40/Fc cDNA which encodes a
CC fusion protein that contains the extracellular domain of mouse OX40
CC fused to the mutated Fc region of the human IgG1 antibody. The
CC fusion protein was used for detecting cDNA clones encoding an OX40
CC ligand. The invention claims for a murine OX40-L cytokine (AAM48975)
CC that binds to the murine T cell antigen, OX40. The OX40-L protein
CC is claimed to be useful for co-stimulation of T-cell production and
CC in binding assays for detecting OX40 or its homologues. The OX40-L
CC protein is also claimed to generate a Th-2 immune response.
XX
SQ Sequence 1317 BP; 322 A; 417 C; 337 G; 241 T; 0 other;

Query Match 2.6%; Score 28; DB 19; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 acaccagcgtcgcaagccctgaccac 451
    |||||||
DB 404 acaacagcgtcgcaagccctgaccac 431

RESULT 14
AAQ93255
ID AAQ93255 standard; DNA: 24 BP.
XX
AC AAQ93255;
XX
DT 21-DEC-1995 (first entry)
XX
DE PCR primer 1 for human OX-40 cDNA.
XX
KW Primer: human OX-40; PCR; ss.
XX
OS Synthetic.
XX
PN WO9521251-A.
XX
PD 10-AUG-1995.
XX
PF 06-FEB-1995; 95WO-GB00237.
XX
PR 04-FEB-1994; 94US-0192480.
XX
PA (WEIN/) WEINBERG A D.
PA (CANT-) CANTAB PHARM RES LTD.
XX
PI Vandenbark AA, Weinberg AD;
XX
DR WPI: 1995-283771/37.
XX
PT Nucleic acid encoding an activated T-cell antigen, OX-40 - used to
PT developed prods. for detection and therapy of conditions mediated by
PT activated T-cells, eg. multiple sclerosis, rheumatoid arthritis, etc.
XX
PS Example; Page 50; 91pp; English.
XX
```

```
CC Antigen OX-40 is specifically expressed on the cell surface of
CC antigen activated T-cells, especially, for example, CD4+ T-cells.
CC A human cDNA encoding the human OX-40 homologue was cloned using
CC primers 1 and 2. Template DNA for PCR amplification to product the
CC human OX-40 cDNA can be extracted from the lambda gill cDNA library
CC from human activated T-lymphocytes produced by Clontech, Palo Alto,
CC California (Catalog No. HL10316).
XX
SQ Sequence 24 BP; 1 A; 5 C; 13 G; 5 T; 0 other;

Query Match 2.3%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 atgtcgtggtggggtcgagcgcgtg 38
    |||||||
DB 1 atgtcgtggtggggtcgagcgcgtg 24

RESULT 15
AAS46585
ID AAS46585 standard; DNA: 5148 BP.
XX
AC AAS46585;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #307.
XX
KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PF 15-MAR-2001; 2001WO-EP02955.
XX
PR 15-MAR-2000; 2000DE-1013847.
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI: 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
PT cancer
XX
PS Claim 1; SEQ ID No 307; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes, having a sequence taken from 536 (actually 533 since
CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a
CC peptide nucleic acid-oligonmer (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms and also to be used in an
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
```

CC and/or therapy of existing diseases or the predisposition to specific
CC diseases, by analysing cytosine methylations. The parameters may be
CC compared to another set of genetic and/or epigenetic parameters, the
CC differences serving as basis for diagnosis and/or prognosis events which
CC are disadvantageous to patients. The present sequence is one of the
CC 533 genomic sequences derived from tumour suppressor genes and
CC oncogenes.
CC Note: The sequence data for this patent did not form part
CC of the printed specification, but was obtained in electronic
CC format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 5148 BP; 871 A; 182 C; 1479 G; 2615 T; 1 other;

Query Match 2.2%; Score 23; DB 22; Length 5148;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 agagacgagatgcgtgaggg 27
|||||
DB 4796 agagacgagatgcgtgaggg 4818

RESULT 16
AAH22273/C
ID AAH22273 standard; DNA; 22 BP.
XX
AC AAH22273;
XX
DT 21-AUG-2001 (first entry)
XX
DE OX40 reverse PCR primer SEQ ID NO:19.
XX
XX Human; differentially expressed gene; angiogenesis; diagnosis;
KM angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
KM vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
KM rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
KM neovascularisation; restenosis; hypertension; aneurysm; angina;
KM myocardial infarction; chronic heart condition; osteoporosis;
KM PCR primer; hybridisation; probe; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200132926-A2.
PN
PD 10-MAY-2001.
XX
XX 01-NOV-2000; 2000WO-US30051.
PF
XX 01-NOV-1999; 99US-0162699.
PR 13-APR-2000; 2000US-0196802.
PR 31-OCT-2000; 2000US-0703350.
XX
PA (CURA-) CURAGEN CORP.
PA (GETH) GENENTECH INC.
PI Mehrahan F, Gerritsen M, Rastelli L;
PI
XX WPI; 2001-291056/30.
DR
XX
XX Differentially expressed genes involved in angiogenesis, useful for
PT treating e.g. vascular tumors, atherosclerosis and/or restenosis
PT subsequent to balloon angioplasty -
XX
XX Example 19; Page 147; 182pp; English.
XX
XX The present invention describes differentially expressed genes involved
CC in angiogenesis (I), and the polypeptides that encode them. (I) have
CC cardiovascular activity, and can be used in the modulation of
CC angiogenesis. The nucleic acids and polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate angiogenesis. The polypeptides may also be used as antigens
CC in the production of antibodies against them and in assays to identify
CC modulators of their expression and activity. The antibodies and
CC antagonists may also be used to down regulate expression and activity
CC and modulate angiogenesis. The antibodies may also be used as diagnostic
CC agents for detecting the presence of the polypeptides in samples.
CC Disorders that may be prevented, diagnosed and/or treated by the above
CC methods include, for example vascular tumours, proliferative tumours,
CC proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
CC associated with neovascularisation, restenosis subsequent to balloon
CC angioplasty, scar tissue over production, peripheral vascular disease,
CC hypertension, inflammatory vasculitides, Reynaud's disease and
CC Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
CC lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
CC reperfusion injury, angina, myocardial infarctions, chronic heart
CC conditions, heart failure such as congestive heart failure, age-related
CC macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322
CC to AAB98325 represent sequence used in the exemplification of the
CC present invention.
XX
SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 2.1%; Score 22; DB 22; Length 22;
Best Local Similarity 100.0%; Pred. No. 5.1;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1001 gcttacctatgcataacc 1022
|||||
DB 22 gcttacctatgcataacc 1

RESULT 17
AAH22272
ID AAH22272 standard; DNA; 21 BP.
XX
AC AAH22272;
XX
DT 21-AUG-2001 (first entry)
XX
DE OX40 forward PCR primer SEQ ID NO:18.
XX
XX Human; differentially expressed gene; angiogenesis; diagnosis;
KM angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
KM vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
KM rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
KM neovascularisation; restenosis; hypertension; aneurysm; angina;
KM myocardial infarction; chronic heart condition; osteoporosis;
KM PCR primer; hybridisation; probe; ss.
XX
XX Homo sapiens.
OS Synthetic.
OS
XX WO200132926-A2.
PN
PD 10-MAY-2001.
XX
XX 01-NOV-2000; 2000WO-US30051.
PF
XX 01-NOV-1999; 99US-0162699.
PR 13-APR-2000; 2000US-0196802.
PR 31-OCT-2000; 2000US-0703350.
XX
PA (CURA-) CURAGEN CORP.
PA (GETH) GENENTECH INC.
PI Mehrahan F, Gerritsen M, Rastelli L;
PI
XX WPI; 2001-291056/30.
DR
XX
XX Differentially expressed genes involved in angiogenesis, useful for
PT treating e.g. vascular tumors, atherosclerosis and/or restenosis

PT subsequent to balloon angioplasty -
 XX
 PS Example 19; Page 147; 182pp; English.
 XX
 CC The present invention describes differentially expressed genes involved
 CC in angiogenesis (I), and the polypeptides that encode them. (I) have
 CC cardiovascular activity, and can be used in the modulation of
 CC angiogenesis. The nucleic acids and polypeptides may be used in the
 CC prevention, diagnosis and treatment of diseases associated with
 CC inappropriate angiogenesis. The polypeptides may also be used as antigens
 CC in the production of antibodies against them and in assays to identify
 CC modulators of their expression and activity. The antibodies and
 CC antagonists may also be used to down regulate expression and activity
 CC and modulate angiogenesis. The antibodies may also be used as diagnostic
 CC agents for detecting the presence of the polypeptides in samples.
 CC Disorders that may be prevented, diagnosed and/or treated by the above
 CC methods include, for example vascular tumours, proliferative tumours,
 CC proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
 CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
 CC associated with neovascularisation, restenosis subsequent to balloon
 CC angioplasty, scar tissue over production, peripheral vascular disease,
 CC hypertension, inflammatory vasculitides, Reynaud's disease and
 CC Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
 CC lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
 CC reperfusion injury, angina, myocardial infarctions, chronic heart
 CC conditions, heart failure such as congestive heart failure, age-related
 CC macular degeneration and osteoporosis. AAH2225 to AAH22325 and AAH98322
 CC to AAH98325 represent sequence used in the exemplification of the
 CC present invention.
 CC
 XX
 SQ Sequence 21 BP; 4 A; 8 C; 4 G; 5 T; 0 other;

Query Match 2.0%; Score 21; DB 22; Length 21;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 955 ccaactctgacccgtctagg 975
 ||||||||||||||||
 DB 1 ccaactctgacccgtctagg 21

RESULT 18
 AAA87680
 ID AAA87680 standard; cDNA; 1153 BP.
 XX
 AC AAA87680;
 DT 04-DEC-2000 (first entry)
 XX
 DE Human secreted protein gene 15 SEQ ID NO:25.
 XX
 KW Human; secreted protein; immunosuppressive; immunostimulant; nootropic;
 KW antiinflammatory; cardiant; vulnerrary; antitumor; anticonvulsant;
 KW antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic;
 KW antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic;
 KW gene therapy; vaccine; chemotaxis-modulator; angiogenesis-modulator;
 KW cancer; immune system disorder; hyperproliferative disorder; infection;
 KW cardiovascular disorder; neurological disease; wound healing;
 KW chromosome 17; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200043495-A2.
 PD 27-JUL-2000.
 PF 18-JAN-2000; 2000WO-US00903.
 XX
 PR 19-JAN-1999; 99US-0116330.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX

PT Rosen CA, Ruben SM, Edner R, Young PE, Ni J, Moore PA;
 PI Komatsoulis G, Birse CE;
 XX
 DR MPI: 2000-499225/44.
 XX
 PS P-PSDB; AAB25679.
 PT New isolated polynucleotide encoding a secreted protein useful for
 preventing, treating or ameliorating a medical condition -
 XX
 PS Claim 1; Page 386; 451pp; English.
 XX
 CC The polynucleotide sequences given in AAA87666 to AAA87708 encodes the
 CC human secreted proteins given in AAB25665 to AAB25755. Human secreted
 CC proteins have activities based on the tissues and cells the genes are
 CC expressed in. Examples of activities include: immunosuppressive;
 CC immunostimulant; antiinflammatory; cardiant; vulnerrary; antitumor;
 CC nootropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective;
 CC antibacterial; antiparasitic; thrombolytic; anticoagulant;
 CC antiarteriosclerotic and cytostatic. The secreted proteins and their
 CC polynucleotides can be used in gene therapy and as vaccines,
 CC chemotaxis-modulators and angiogenesis-modulators. The human secreted
 CC proteins and polynucleotides can be used for diagnosing (the
 CC susceptibility to) a pathological condition by determining the presence
 CC or absence of a mutation in the polynucleotide or determining the
 CC presence or amount of expression of the protein. The polynucleotides and
 CC proteins can also be used in the treatment and diagnosis of cancer,
 CC diseases of the immune system, hyperproliferative disorders,
 CC cardiovascular disorders and neurological disease. They can also be used
 CC to promote wound healing and to fight infection. AAA87657 to AAA87665 and
 CC AAB25664 represent sequences used in the exemplification of the present
 CC invention.
 CC
 XX
 SQ Sequence 1153 BP; 241 A; 376 C; 279 G; 255 T; 2 other;

Query Match 2.0%; Score 21; DB 21; Length 1153;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 688 tggggctgctgggccccctgg 708
 ||||||||||||||||
 DB 638 tggggctgctgggccccctgg 658

RESULT 19
 AAC76846
 ID AAC76846 standard; cDNA; 1447 BP.
 XX
 AC AAC76846;
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF2401 polynucleotide sequence SEQ ID NO:4801.
 XX
 KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;
 KW vulnerrary; antiparasitic; antiparkinsonian; nootropic; neuroprotective;
 KW immunostimulant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;
 KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200058473-A2.
 XX

PD	05-OCT-2000.
XX	
PE	31-MAR-2000; 2000WO-US08621.
XX	
PR	31-MAR-1999; 9905-0127607.
PR	02-APR-1999; 9905-0127636.
PR	05-APR-1999; 9905-0127728.
PR	30-MAR-2000; 2000US-0540763.
XX	
PA	(CURA-) CURAGEN CORP.
XX	
PI	Shimkets RA, Leach M;
DR	WPI; 2000-602362/57.
DR	P-PSDB; AAB42637.
XX	
PT	Novel nucleic acids and peptides derived from open reading frame X,
PT	useful for treating e.g. cancers, proliferative disorders,
XX	neurodegenerative disorders and cardiovascular disease -
XX	
PS	Claim 5; Page 3984-3985; 5507pp; English.
XX	
CC	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
CC	which represent the human ORFX open reading frames 1 to 3161. The ORFX
CC	sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC	antiproliferic; antiparkinsonian; neurotropic; neuroprotective;
CC	osteoparitic; anticonvulsant; antiallergic; immunosuppressant;
CC	immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC	antidiabetic; hypotensive; dermatological; antiviral; immunosuppressive;
CC	antiflammatory; antibacterial; antiviral; antifungal; antirheumatic;
CC	antihypoid; and antianemic. The sequences can be used for determining
CC	the presence of or predisposition to, or preventing or treating
CC	pathological conditions associated with an ORFX-associated disorder. The
CC	nucleic acids can be used to express ORFX proteins in gene therapy
CC	vectors. The proteins and nucleic acids may be used to treat cancers,
CC	proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC	graft vs host disease, cardiovascular disease, diabetes mellitus,
CC	hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC	erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC	bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC	allergies, aplastic anemia, burns, wounds, bone and cartilage damage,
CC	nocturnal haemoglobinuria, antinflammatory disease; to enhance
CC	coagulation; to inhibit thrombosis; and as a contraceptive.
XX	
SQ	Sequence 1447 BP: 250 A; 477 C; 376 G; 341 T; 3 other:
XX	
Query Match	2.0%; Score 21; DB 21; Length 1447;
Best Local Similarity	100.0%; Pred. No. 10;
Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	688 tggggctgctggggccctctg 708
Db	965 tggggctgctggggccctctg 985
XX	
RESULT	20
AAK52633	
ID	AAK52633 standard; cDNA; 1461 BP.
XX	
AAK52633:	
XX	
DT	06-NOV-2001 (first entry)
XX	
DE	Human polynucleotide SEQ ID NO 2162.
XX	
KW	Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW	vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW	tissue growth factor; immunomodulatory; cancer; leukemia;
KW	nervous system disorder; arthritis; inflammation; ss.
XX	
SS	homo sapiens
XX	

FN	MO200157190-A2.
PD	09-AUG-2001.
XX	
PF	05-FEB-2001; 2001WO-US04098.
XX	
PR	03-FEB-2000; 2000US-0496914.
PR	27-APR-2000; 2000US-0560875.
PR	20-JUN-2000; 2000US-0598075.
PR	19-JUL-2000; 2000US-0620325.
PR	01-SEP-2000; 2000US-0634936.
PR	15-SEP-2000; 2000US-0663561.
PR	20-OCT-2000; 2000US-0693325.
PR	30-NOV-2000; 2000US-0728422.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Tang YT, Liu C, Dimanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI	Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI	Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX	
DR	WPI: 2001-476283/51.
DR	P-PSDB; AAM79500.
XX	
PT	Nucleic acids encoding polypeptides with cytokine-like activities,
PT	useful in diagnosis and gene therapy -
XX	
PS	Claim 1; Page 4529; 6221pp; English.
XX	
CC	The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC	encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC	cytokine, cell proliferation or cell differentiation or which may induce
CC	production of other cytokines in other cell populations. The
CC	polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC	peptide therapeutics. The polypeptides have various cytokine-like activities,
CC	e.g. stem cell growth factor activity, haematopoiesis regulating
CC	activity, tissue growth factor activity, immunomodulatory activity and
CC	activin/inhibin activity and may be useful in the diagnosis and/or
CC	treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC	inflammation.
CC	Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC	(AAM80020) are omitted as the relevant pages from the sequence listing
CC	were missing at the time of publication.
XX	
SO	Sequence 1461 BP; 249 A; 487 C; 382 G; 343 T; 0 other:
	Query Match 2.0%; Score 21; DB 22; Length 1461;
	Best Local Similarity 100.0%; Pred. No. 10;
	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	688 tgggagctgctggccctcg 708
Db	982 tgggagctgctggccctcg 1002
RESULT 21	
AAH22958	
ID	AAH22958 standard; cDNA: 1569 BP.
XX	
AC	AAH22958;
XX	
DT	17-SEP-2001 (first entry)
XX	
DE	Human phosphatase (PP) encoding cDNA (clone ID 1269556CB1).
XX	
KW	Phosphatase; PP; Alzheimer's disease; Huntington's disease; human;
KW	immune disorder; cancer; neurotropic; immunomodulatory; cyostatic;
KW	neuroprotective; anticonvulsant; ss.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
XX	

```
FT CDS 218..1375
FT /*tag= a
FT /product= "phosphatase"
XX
XX WO200153469-A2.
XX
XX 26-JUL-2001.
XX
XX 18-JAN-2001; 2001WO-US02088.
XX
XX 21-JAN-2000; 2000US-0177719.
XX 28-JAN-2000; 2000US-0178988.
XX 25-FEB-2000; 2000US-0184959.
XX 17-MAR-2000; 2000US-0190142.
XX
XX (INCYTE GENOMICS INC.
XX
XX Bandman O, Tang YT, Azimzal Y, Yue H, Baughn MR, Hillman JL;
XX Lal P, Wang E, Gandhl AR, Policky JL, Mathur P;
XX
XX WPI: 2001-451905/48.
XX P-PSDB; AAB85355.
XX
XX Novel phosphatases useful for treating diseases associated with
XX decreased expression of functional phosphatases, e.g., Alzheimer's
XX disease, Huntington's disease, immune disorders, and cancers -
XX
XX Claim 5; Page 98-99; 103pp; English.
XX
XX The invention provides human phosphatases (PP) and polynucleotides
XX encoding the phosphatases. The polypeptides can be expressed by standard
XX recombinant methodology. The PP are useful for treating a disease or
XX condition associated with decreased expression of functional
XX phosphatases. Compositions containing agonists or antagonists of PP may
XX be used to treat a disease associated with decreased expression or
XX overexpression of PP, respectively. Such diseases may include
XX Alzheimer's disease, Huntington's disease, immune disorders, and
XX cancers. The present sequence represents a human phosphatase encoding
XX cDNA.
XX
XX Sequence 1569 BP; 263 A; 505 C; 444 G; 357 T; 0 other:
XX
XX
XX Query Match 2.0%; Score 21; DB 22; Length 1569;
XX Best Local Similarity 100.0%; Pred. No. 9.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 688 tggggctgctgggcccctgg 708
XX ||||||||||||||||||||
XX Db 1089 tggggctgctgggcccctgg 1109
XX
XX
XX RESULT 22
XX AAK51649
XX ID AAK51649 standard; cDNA; 1658 BP.
XX
XX AAK51649;
XX
XX 06-NOV-2001 (first entry)
XX
XX Human polynucleotide SEQ ID NO 194.
XX
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorder; arthritis; inflammation; ss.
XX
XX Homo sapiens.
XX
XX WO200157190-A2.
XX
XX 09-AUG-2001.
XX
```

```
PF 05-FEB-2001; 2001WO-US04098.
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
XX Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
XX WPI: 2001-476283/51.
XX P-PSDB; AAM78516.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX Claim 1; Page 981-983; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 1658 BP; 282 A; 536 C; 499 G; 341 T; 0 other:
XX
XX
XX Query Match 2.0%; Score 21; DB 22; Length 1658;
XX Best Local Similarity 100.0%; Pred. No. 9.9;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 688 tggggctgctgggcccctgg 708
XX ||||||||||||||||||||
XX Db 1178 tggggctgctgggcccctgg 1198
XX
XX
XX RESULT 23
XX AAL36023/C
XX ID AAL36023 standard; DNA; 5808 BP.
XX
XX AAL36023;
XX
XX 08-JAN-2002 (first entry)
XX
XX Human musculoskeletal system related polynucleotide SEQ ID NO 2388.
XX
XX Cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;
XX antiallergic; hepatotropic; antidiabetic; antiinflammatory; antiulcer;
XX vulnerrary; anticonvulsant; antibacterial; antifungal; antiparasitic;
XX cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder;
XX neurological disease; infection; human; secreted protein;
XX musculoskeletal system; ds.
XX
XX Homo sapiens.
XX
XX WO200155367-A1.
XX
```

PD	02-AUG-2001.	
XX	17-JAN-2001;	2001WO-US01338
XX	31-JAN-2000;	2000US-0179065
PR	04-FEB-2000;	2000US-0180660
PR	24-FEB-2000;	2000US-0186864
PR	02-MAR-2000;	2000US-0186504
PR	16-MAR-2000;	2000US-0186874
PR	17-MAR-2000;	2000US-0190076
PR	18-APR-2000;	2000US-0195123
PR	19-MAY-2000;	2000US-0205155
PR	07-JUN-2000;	2000US-0209467
PR	28-JUN-2000;	2000US-0214886
PR	30-JUL-2000;	2000US-0215135
PR	07-JUL-2000;	2000US-0216647
PR	07-JUL-2000;	2000US-0216880
PR	11-JUL-2000;	2000US-0217487
PR	11-JUL-2000;	2000US-0217496
PR	14-JUL-2000;	2000US-0218293
PR	26-JUL-2000;	2000US-0220964
PR	26-JUL-2000;	2000US-0220964
PR	14-AUG-2000;	2000US-0224518
PR	14-AUG-2000;	2000US-0224519
PR	14-AUG-2000;	2000US-0225213
PR	14-AUG-2000;	2000US-0225214
PR	14-AUG-2000;	2000US-0225266
PR	14-AUG-2000;	2000US-0225267
PR	14-AUG-2000;	2000US-0225268
PR	14-AUG-2000;	2000US-0225270
PR	14-AUG-2000;	2000US-0225347
PR	14-AUG-2000;	2000US-0225357
PR	14-AUG-2000;	2000US-0225758
PR	14-AUG-2000;	2000US-0225759
PR	18-AUG-2000;	2000US-0226279
PR	22-AUG-2000;	2000US-0226681
PR	22-AUG-2000;	2000US-0226686
PR	22-AUG-2000;	2000US-0227182
PR	23-AUG-2000;	2000US-0227024
PR	23-AUG-2000;	2000US-0228924
PR	01-SEP-2000;	2000US-0229287
PR	01-SEP-2000;	2000US-0229287
PR	01-SEP-2000;	2000US-0229344
PR	01-SEP-2000;	2000US-0229345
PR	05-SEP-2000;	2000US-0229509
PR	05-SEP-2000;	2000US-0229513
PR	06-SEP-2000;	2000US-0230348
PR	08-SEP-2000;	2000US-0231242
PR	08-SEP-2000;	2000US-0231243
PR	08-SEP-2000;	2000US-0231244
PR	08-SEP-2000;	2000US-0231413
PR	08-SEP-2000;	2000US-0231414
PR	08-SEP-2000;	2000US-0233080
PR	12-SEP-2000;	2000US-0233081
PR	12-SEP-2000;	2000US-0233196
PR	14-SEP-2000;	2000US-0233063
PR	14-SEP-2000;	2000US-0233064
PR	14-SEP-2000;	2000US-0233065
PR	21-SEP-2000;	2000US-0234273
PR	21-SEP-2000;	2000US-0234274
PR	25-SEP-2000;	2000US-0234597
PR	25-SEP-2000;	2000US-0234598
PR	26-SEP-2000;	2000US-0235484
PR	27-SEP-2000;	2000US-0235834
PR	27-SEP-2000;	2000US-0235836
PR	29-SEP-2000;	2000US-0235327
PR	29-SEP-2000;	2000US-0235327

PR	29-SEP-2000	2000US-0236368
PR	29-SEP-2000	2000US-0236369
PR	29-SEP-2000	2000US-0236370
PR	02-OCT-2000	2000US-0236802
PR	02-OCT-2000	2000US-0237037
PR	02-OCT-2000	2000US-0237038
PR	02-OCT-2000	2000US-0237039
PR	12-OCT-2000	2000US-0237940
PR	13-OCT-2000	2000US-0239935
PR	13-OCT-2000	2000US-0239937
PR	20-OCT-2000	2000US-0240960
PR	20-OCT-2000	2000US-0241121
PR	20-OCT-2000	2000US-0241785
PR	20-OCT-2000	2000US-0241786
PR	20-OCT-2000	2000US-0241787
PR	20-OCT-2000	2000US-0241808
PR	20-OCT-2000	2000US-0241809
PR	01-NOV-2000	2000US-0244186
PR	01-NOV-2000	2000US-0244617
PR	08-NOV-2000	2000US-0246474
PR	08-NOV-2000	2000US-0246475
PR	08-NOV-2000	2000US-0246526
PR	08-NOV-2000	2000US-0246527
PR	08-NOV-2000	2000US-0246528
PR	08-NOV-2000	2000US-0246532
PR	08-NOV-2000	2000US-0246609
PR	08-NOV-2000	2000US-0246610
PR	08-NOV-2000	2000US-0246611
PR	08-NOV-2000	2000US-0246613
PR	17-NOV-2000	2000US-0249207
PR	17-NOV-2000	2000US-0249208
PR	17-NOV-2000	2000US-0249209
PR	17-NOV-2000	2000US-0249210
PR	17-NOV-2000	2000US-0249211
PR	17-NOV-2000	2000US-0249212
PR	17-NOV-2000	2000US-0249213
PR	17-NOV-2000	2000US-0249214
PR	17-NOV-2000	2000US-0249215
PR	17-NOV-2000	2000US-0249216
PR	17-NOV-2000	2000US-0249217
PR	17-NOV-2000	2000US-0249218
PR	17-NOV-2000	2000US-0249219
PR	17-NOV-2000	2000US-0249224
PR	17-NOV-2000	2000US-0249245
PR	17-NOV-2000	2000US-0249264
PR	17-NOV-2000	2000US-0249265
PR	17-NOV-2000	2000US-0249267
PR	17-NOV-2000	2000US-0249268
PR	17-NOV-2000	2000US-0249269
PR	17-NOV-2000	2000US-0249270
PR	17-NOV-2000	2000US-0249271
PR	17-NOV-2000	2000US-0249272
PR	17-NOV-2000	2000US-0249273
PR	17-NOV-2000	2000US-0249274
PR	17-NOV-2000	2000US-0249275
PR	17-NOV-2000	2000US-0249276
PR	17-NOV-2000	2000US-0249277
PR	17-NOV-2000	2000US-0249278
PR	17-NOV-2000	2000US-0249279
PR	17-NOV-2000	2000US-0249280
PR	17-NOV-2000	2000US-0249281
PR	17-NOV-2000	2000US-0249282
PR	17-NOV-2000	2000US-0249283
PR	17-NOV-2000	2000US-0249284
PR	17-NOV-2000	2000US-0249285
PR	17-NOV-2000	2000US-0249286
PR	17-NOV-2000	2000US-0249287
PR	17-NOV-2000	2000US-0249288
PR	17-NOV-2000	2000US-0249289
PR	17-NOV-2000	2000US-0249290
PR	17-NOV-2000	2000US-0249291
PR	17-NOV-2000	2000US-0249292
PR	17-NOV-2000	2000US-0249293
PR	17-NOV-2000	2000US-0249294
PR	17-NOV-2000	2000US-0249295
PR	17-NOV-2000	2000US-0249296
PR	17-NOV-2000	2000US-0249297
PR	17-NOV-2000	2000US-0249298
PR	17-NOV-2000	2000US-0249299
PR	17-NOV-2000	2000US-0249300
PR	01-DEC-2000	2000US-0250160
PR	01-DEC-2000	2000US-0250161
PR	01-DEC-2000	2000US-0250191
PR	05-DEC-2000	2000US-0251030
PR	05-DEC-2000	2000US-0251068
PR	05-DEC-2000	2000US-0251198
PR	05-DEC-2000	2000US-0256719
PR	06-DEC-2000	2000US-0251479
PR	06-DEC-2000	2000US-0251485
PR	08-DEC-2000	2000US-0251668
PR	08-DEC-2000	2000US-0251669
PR	08-DEC-2000	2000US-0251688
PR	08-DEC-2000	2000US-0251689
PR	08-DEC-2000	2000

XX Isolated polypeptide for treating, preventing and/or prognosing
PR disorders related to the musculoskeletal system including
PR musculoskeletal cancers and also for testing and detection e.g.
PR diagnosis -
XX
PS Example 2; SEQ ID NO 2388; 781bp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 5808 BP; 1521 A; 1464 C; 1655 G; 1168 T; 0 other;

Query Match 2.0%; Score 21; DB 22; Length 5808;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 688 tggggctgctgggccccctgg 708
|||||
Db 471 TGGGGCTGCTGGGCCCCCTGG 451

RESULT 24
ID AAK69724 standard; DNA; 5808 BP.
XX
AC AAK69724;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24536.
XX
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0188874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.

PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226686.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235836.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.
PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.

PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-024617.
PR 08-NOV-2000; 2000US-0246174.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246613.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
PI
XX WPI; 2001-483426/52.
XX
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
PT useful for preventing, diagnosing and/or treating cancers and
PT metastasis -
XX
XX
PS Disclosure; SEQ ID NO 24536; 3071pp + Sequence Listing; English.
XX
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I) to

CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 5808 BP; 1168 A; 1655 C; 1464 G; 1521 T; 0 other;

Query Match 2.0%; Score 21; DB 22; Length 5808;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgctgggcccctgg 708
Db 5338 tggggctgctgggcccctgg 5358.

RESULT 25
AAK84953
ID AAK84953 standard; DNA; 38348 BP.
XX
AC AAK84953;
XX
DT 07-NOV-2001 (first entry)
XX
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:39765.
XX
KW Human; immune; haematopoietic; immune/hematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
OS Homo sapiens.
XX
PN WO200157182-A2.
XX
PD 09-AUG-2001.
XX
PE
PF 17-JAN-2001; 2001WO-US01354.
XX
PR 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
PR 24-FEB-2000; 2000US-0184564.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.

PR 22-AUG-2000; 2000US-0226681.
 PR 22-AUG-2000; 2000US-0226868.
 PR 22-AUG-2000; 2000US-0227182.
 PR 23-AUG-2000; 2000US-0227009.
 PR 30-AUG-2000; 2000US-0228924.
 PR 01-SEP-2000; 2000US-0229287.
 PR 01-SEP-2000; 2000US-0229343.
 PR 01-SEP-2000; 2000US-0229344.
 PR 01-SEP-2000; 2000US-0229345.
 PR 05-SEP-2000; 2000US-0229509.
 PR 05-SEP-2000; 2000US-0229513.
 PR 06-SEP-2000; 2000US-0230437.
 PR 06-SEP-2000; 2000US-0230438.
 PR 08-SEP-2000; 2000US-0231242.
 PR 08-SEP-2000; 2000US-0231243.
 PR 08-SEP-2000; 2000US-0231244.
 PR 08-SEP-2000; 2000US-0231413.
 PR 08-SEP-2000; 2000US-0231414.
 PR 08-SEP-2000; 2000US-0232080.
 PR 12-SEP-2000; 2000US-0232081.
 PR 14-SEP-2000; 2000US-0232397.
 PR 14-SEP-2000; 2000US-0232398.
 PR 14-SEP-2000; 2000US-0232399.
 PR 14-SEP-2000; 2000US-0232400.
 PR 14-SEP-2000; 2000US-0232401.
 PR 14-SEP-2000; 2000US-0233063.
 PR 14-SEP-2000; 2000US-0233064.
 PR 14-SEP-2000; 2000US-0233065.
 PR 21-SEP-2000; 2000US-0234223.
 PR 21-SEP-2000; 2000US-0234274.
 PR 25-SEP-2000; 2000US-0234997.
 PR 25-SEP-2000; 2000US-0234998.
 PR 26-SEP-2000; 2000US-0234984.
 PR 27-SEP-2000; 2000US-0235834.
 PR 27-SEP-2000; 2000US-0235836.
 PR 29-SEP-2000; 2000US-0236327.
 PR 29-SEP-2000; 2000US-0236367.
 PR 29-SEP-2000; 2000US-0236368.
 PR 29-SEP-2000; 2000US-0236369.
 PR 29-SEP-2000; 2000US-0236370.
 PR 02-OCT-2000; 2000US-0236802.
 PR 02-OCT-2000; 2000US-0237037.
 PR 02-OCT-2000; 2000US-0237038.
 PR 02-OCT-2000; 2000US-0237039.
 PR 02-OCT-2000; 2000US-0237040.
 PR 13-OCT-2000; 2000US-0239935.
 PR 13-OCT-2000; 2000US-0239937.
 PR 20-OCT-2000; 2000US-0240960.
 PR 20-OCT-2000; 2000US-0241221.
 PR 20-OCT-2000; 2000US-0241785.
 PR 20-OCT-2000; 2000US-0241786.
 PR 20-OCT-2000; 2000US-0241787.
 PR 20-OCT-2000; 2000US-0241808.
 PR 20-OCT-2000; 2000US-0241809.
 PR 20-OCT-2000; 2000US-0241826.
 PR 01-NOV-2000; 2000US-0244617.
 PR 08-NOV-2000; 2000US-0246474.
 PR 08-NOV-2000; 2000US-0246475.
 PR 08-NOV-2000; 2000US-0246476.
 PR 08-NOV-2000; 2000US-0246477.
 PR 08-NOV-2000; 2000US-0246478.
 PR 08-NOV-2000; 2000US-0246523.
 PR 08-NOV-2000; 2000US-0246524.
 PR 08-NOV-2000; 2000US-0246525.
 PR 08-NOV-2000; 2000US-0246526.
 PR 08-NOV-2000; 2000US-0246527.
 PR 08-NOV-2000; 2000US-0246528.
 PR 08-NOV-2000; 2000US-0246532.
 PR 08-NOV-2000; 2000US-0246609.
 PR 08-NOV-2000; 2000US-0246610.
 PR 08-NOV-2000; 2000US-0246611.
 PR 08-NOV-2000; 2000US-0246613.

PR 17-NOV-2000; 2000US-0249207.
 PR 17-NOV-2000; 2000US-0249208.
 PR 17-NOV-2000; 2000US-0249209.
 PR 17-NOV-2000; 2000US-0249210.
 PR 17-NOV-2000; 2000US-0249211.
 PR 17-NOV-2000; 2000US-0249212.
 PR 17-NOV-2000; 2000US-0249213.
 PR 17-NOV-2000; 2000US-0249214.
 PR 17-NOV-2000; 2000US-0249215.
 PR 17-NOV-2000; 2000US-0249216.
 PR 17-NOV-2000; 2000US-0249217.
 PR 17-NOV-2000; 2000US-0249218.
 PR 17-NOV-2000; 2000US-0249244.
 PR 17-NOV-2000; 2000US-0249245.
 PR 17-NOV-2000; 2000US-0249246.
 PR 17-NOV-2000; 2000US-0249265.
 PR 17-NOV-2000; 2000US-0249266.
 PR 17-NOV-2000; 2000US-0249297.
 PR 17-NOV-2000; 2000US-0249299.
 PR 01-DEC-2000; 2000US-0250160.
 PR 01-DEC-2000; 2000US-0250391.
 PR 05-DEC-2000; 2000US-0251030.
 PR 05-DEC-2000; 2000US-0251988.
 PR 05-DEC-2000; 2000US-0256719.
 PR 06-DEC-2000; 2000US-0251479.
 PR 08-DEC-2000; 2000US-0251856.
 PR 08-DEC-2000; 2000US-0251869.
 PR 08-DEC-2000; 2000US-0251989.
 PR 08-DEC-2000; 2000US-0251990.
 PR 11-DEC-2000; 2000US-0254097.
 PR 05-JAN-2001; 2001US-0259678.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI Rosen CA, Barash SC, Ruben SM;
 XX WPI: 2001-483426/52.
 XX
 DR Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating cancers and
 PT metastasis -
 PT
 PT
 PT
 XX
 XX
 PS Disclosure; SEQ ID NO 39765; 3071bp + Sequence Listing; English.
 PS
 XX
 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic
 CC activity, and can be used in gene therapy and vaccine production. (I)
 CC proteins and polynucleotides may be used in the prevention, diagnosis and
 CC treatment of diseases associated with inappropriate (I) expression. For
 CC example, they may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of (I) by expressing inactive proteins or to
 CC supplement the patient's own production of (I). Additionally, (I)
 CC polynucleotides may be used to produce the secreted (I), by inserting
 CC the nucleic acids into a host cell and culturing the cell to express the
 CC protein. (I) proteins and polynucleotides may be used to prevent,
 CC diagnose and treat immune/hematopoietic-related diseases, especially
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703
 CC to AAK87694 represent human immune/hematopoietic antigen genomic
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169
 CC represent sequences used in the exemplification of the present invention.
 CC
 XX
 XX
 SQ Sequence 38348 BP; 9411 A; 7405 C; 8303 G; 13229 T; 0 other;

Query Match 2.0%; Score 21; DB 22; Length 38348;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 684 gtgcctggggctgctggggccccc 704
 |||||||||||||||||||||
 Db 34516 gtgcctggggctgctggggccccc 34536

```
RESULT 26
ABL17164
ID ABL17164 standard; DNA; 4466 BP.
XX
XX ABL17164;
AC
XX
XX 26-MAR-2002 (first entry)
DE Drosophila melanogaster genomic polynucleotide SEQ ID NO 2965.
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
XX pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI: 2001-656860/75.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 2965; 21bp + sequence listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX
XX (AB57737-AB872072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 4466 BP; 1312 A; 945 C; 916 G; 1293 T; 0 other;

Query Match 1.9%; Score 20; DB 23; Length 4466;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 gctctgcttacctatgcc 1013
DB 186 gctctgcttacctatgcc 205

RESULT 27
ABL15756
ID ABL15756 standard; cDNA; 6361 BP.
XX
XX ABL15756;
AC
XX
XX 26-MAR-2002 (first entry)
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 41750.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
XX
```

```
XX pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
XX
XX WO200171042-A2.
XX
XX 27-SEP-2001.
XX
XX 23-MAR-2001; 2001WO-US09231.
XX
XX 23-MAR-2000; 2000US-191637P.
XX
XX 11-JUL-2000; 2000US-0614150.
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI: 2001-656860/75.
XX
XX P-PSDB; ABB71653.
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
XX genes from Drosophila and for elucidating cell signalling and cell-cell
XX interactions -
XX
XX Claim 1; SEQ ID NO 41750; 21bp + sequence listing; English.
XX
XX The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX
XX (AB57737-AB872072).
XX
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 6361 BP; 1759 A; 1273 C; 1395 G; 1934 T; 0 other;

Query Match 1.9%; Score 20; DB 23; Length 6361;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 994 gctctgcttacctatgcc 1013
DB 5437 gctctgcttacctatgcc 5456

RESULT 28
AAK84952
ID AAK84952 standard; DNA; 38272 BP.
XX
XX AAK84952;
AC
XX
XX 07-NOV-2001 (first entry)
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39764.
DE
XX
XX Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX
XX cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
XX
XX WO200157182-A2.
XX
XX 09-AUG-2001.
XX
XX 17-JAN-2001; 2001WO-US01354.
XX
XX 31-JAN-2000; 2000US-0179065.
XX
XX 04-FEB-2000; 2000US-0180628.
XX
```

PR 24-FEB-2000; 2000US-0184664.
PR 02-MAR-2000; 2000US-0186350.
PR 16-MAR-2000; 2000US-0189874.
PR 17-MAR-2000; 2000US-0190076.
PR 18-APR-2000; 2000US-0198123.
PR 19-MAY-2000; 2000US-0205515.
PR 07-JUN-2000; 2000US-0209467.
PR 28-JUN-2000; 2000US-0214886.
PR 30-JUN-2000; 2000US-0215135.
PR 07-JUL-2000; 2000US-0216647.
PR 07-JUL-2000; 2000US-0216880.
PR 11-JUL-2000; 2000US-0217487.
PR 11-JUL-2000; 2000US-0217496.
PR 14-JUL-2000; 2000US-0218290.
PR 26-JUL-2000; 2000US-0220963.
PR 26-JUL-2000; 2000US-0220964.
PR 14-AUG-2000; 2000US-0224518.
PR 14-AUG-2000; 2000US-0224519.
PR 14-AUG-2000; 2000US-0225213.
PR 14-AUG-2000; 2000US-0225214.
PR 14-AUG-2000; 2000US-0225266.
PR 14-AUG-2000; 2000US-0225267.
PR 14-AUG-2000; 2000US-0225268.
PR 14-AUG-2000; 2000US-0225270.
PR 14-AUG-2000; 2000US-0225447.
PR 14-AUG-2000; 2000US-0225757.
PR 14-AUG-2000; 2000US-0225758.
PR 14-AUG-2000; 2000US-0225759.
PR 18-AUG-2000; 2000US-0226279.
PR 22-AUG-2000; 2000US-0226681.
PR 22-AUG-2000; 2000US-0226868.
PR 22-AUG-2000; 2000US-0227182.
PR 23-AUG-2000; 2000US-0227009.
PR 30-AUG-2000; 2000US-0228924.
PR 01-SEP-2000; 2000US-0229287.
PR 01-SEP-2000; 2000US-0229343.
PR 01-SEP-2000; 2000US-0229344.
PR 01-SEP-2000; 2000US-0229345.
PR 05-SEP-2000; 2000US-0229509.
PR 05-SEP-2000; 2000US-0229513.
PR 06-SEP-2000; 2000US-0230437.
PR 06-SEP-2000; 2000US-0230438.
PR 08-SEP-2000; 2000US-0231242.
PR 08-SEP-2000; 2000US-0231243.
PR 08-SEP-2000; 2000US-0231244.
PR 08-SEP-2000; 2000US-0231413.
PR 08-SEP-2000; 2000US-0231414.
PR 08-SEP-2000; 2000US-0232080.
PR 08-SEP-2000; 2000US-0232081.
PR 12-SEP-2000; 2000US-0231968.
PR 14-SEP-2000; 2000US-0232397.
PR 14-SEP-2000; 2000US-0232398.
PR 14-SEP-2000; 2000US-0232399.
PR 14-SEP-2000; 2000US-0232400.
PR 14-SEP-2000; 2000US-0232401.
PR 14-SEP-2000; 2000US-0233063.
PR 14-SEP-2000; 2000US-0233064.
PR 14-SEP-2000; 2000US-0233065.
PR 21-SEP-2000; 2000US-0234223.
PR 21-SEP-2000; 2000US-0234274.
PR 25-SEP-2000; 2000US-0234997.
PR 25-SEP-2000; 2000US-0234998.
PR 26-SEP-2000; 2000US-0235484.
PR 27-SEP-2000; 2000US-0235834.
PR 27-SEP-2000; 2000US-0235835.
PR 29-SEP-2000; 2000US-0236327.
PR 29-SEP-2000; 2000US-0236367.
PR 29-SEP-2000; 2000US-0236368.
PR 29-SEP-2000; 2000US-0236369.
PR 29-SEP-2000; 2000US-0236370.
PR 02-OCT-2000; 2000US-0236802.
PR 02-OCT-2000; 2000US-0237037.
PR 02-OCT-2000; 2000US-0237038.

PR 02-OCT-2000; 2000US-0237039.
PR 02-OCT-2000; 2000US-0237040.
PR 13-OCT-2000; 2000US-0239935.
PR 13-OCT-2000; 2000US-0239937.
PR 20-OCT-2000; 2000US-0240960.
PR 20-OCT-2000; 2000US-0241221.
PR 20-OCT-2000; 2000US-0241785.
PR 20-OCT-2000; 2000US-0241786.
PR 20-OCT-2000; 2000US-0241787.
PR 20-OCT-2000; 2000US-0241808.
PR 20-OCT-2000; 2000US-0241809.
PR 20-OCT-2000; 2000US-0241826.
PR 01-NOV-2000; 2000US-0244617.
PR 08-NOV-2000; 2000US-0246474.
PR 08-NOV-2000; 2000US-0246475.
PR 08-NOV-2000; 2000US-0246476.
PR 08-NOV-2000; 2000US-0246477.
PR 08-NOV-2000; 2000US-0246478.
PR 08-NOV-2000; 2000US-0246523.
PR 08-NOV-2000; 2000US-0246524.
PR 08-NOV-2000; 2000US-0246525.
PR 08-NOV-2000; 2000US-0246526.
PR 08-NOV-2000; 2000US-0246527.
PR 08-NOV-2000; 2000US-0246528.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246532.
PR 08-NOV-2000; 2000US-0246609.
PR 08-NOV-2000; 2000US-0246610.
PR 08-NOV-2000; 2000US-0246611.
PR 08-NOV-2000; 2000US-0246611.
PR 17-NOV-2000; 2000US-0249207.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249208.
PR 17-NOV-2000; 2000US-0249209.
PR 17-NOV-2000; 2000US-0249210.
PR 17-NOV-2000; 2000US-0249211.
PR 17-NOV-2000; 2000US-0249212.
PR 17-NOV-2000; 2000US-0249213.
PR 17-NOV-2000; 2000US-0249214.
PR 17-NOV-2000; 2000US-0249215.
PR 17-NOV-2000; 2000US-0249216.
PR 17-NOV-2000; 2000US-0249217.
PR 17-NOV-2000; 2000US-0249218.
PR 17-NOV-2000; 2000US-0249244.
PR 17-NOV-2000; 2000US-0249245.
PR 17-NOV-2000; 2000US-0249264.
PR 17-NOV-2000; 2000US-0249265.
PR 17-NOV-2000; 2000US-0249297.
PR 17-NOV-2000; 2000US-0249299.
PR 17-NOV-2000; 2000US-0249300.
PR 01-DEC-2000; 2000US-0250160.
PR 01-DEC-2000; 2000US-0250391.
PR 05-DEC-2000; 2000US-0251030.
PR 05-DEC-2000; 2000US-0251988.
PR 05-DEC-2000; 2000US-0256719.
PR 06-DEC-2000; 2000US-0251479.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251856.
PR 08-DEC-2000; 2000US-0251868.
PR 08-DEC-2000; 2000US-0251869.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-02559678.

(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-483426/52.
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and
metastasis -
Disclosure; SEQ ID NO 39764; 3071pp + Sequence Listing; English.
PS XX

XX AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patient's own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting the
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/haematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/haematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX

SQ Sequence 38272 BP; 9399 A; 7384 C; 8269 G; 13220 T; 0 other;

Query Match 1.9%; Score 20; DB 22; Length 38272;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 684 gtgctgggctgctggccc 703
|||||
DB 34448 gtgctgggctgctggccc 34467

RESULT 29
AAH22274
ID AAH22274 standard; DNA; 19 BP.

XX AAH22274;
XX
DT 21-AUG-2001 (first entry)

DE OX40 hybridisation probe SEQ ID NO:20.

XX Human; differentially expressed gene; angiogenesis; diagnosis;
KM angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;
KM vascular tumour; proliferative tumour; proliferative vitreoretinopathy;
KM rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;
KM neovascularisation; restenosis; hypertension; aneurysm; angina;
KM myocardial infarction; chronic heart condition; osteoporosis;
KM PCR primer; hybridisation; probe; ss.

XX Homo sapiens.
OS Synthetic.

XX WO200132926-A2.

XX 10-MAY-2001.

PD 01-NOV-2000; 2000MO-US30051.

XX 01-NOV-1999; 99US-0162699.

PR 13-APR-2000; 2000US-0196802.

PR 31-OCT-2000; 2000US-0703350.

XX (CURA-) CURAGEN CORP.

PA (GERTH) GENENTECH INC.

XX Mehraban F, Gerltzen M, Rastelli L;

DR WPI; 2001-291056/30.

XX Differentially expressed genes involved in angiogenesis, useful for
PT treating e.g. vascular tumors, atherosclerosis and/or restenosis
PT subsequent to balloon angioplasty -
XX

PS Example 19; Page 147; 182pp; English.

XX The present invention describes differentially expressed genes involved
CC in angiogenesis (I), and the polypeptides that encode them. (I) have
CC cardiovascular activity, and can be used in the modulation of
CC angiogenesis. The nucleic acids and polypeptides may be used in the
CC prevention, diagnosis and treatment of diseases associated with the
CC inappropriate angiogenesis. The polypeptides may also be used as antigens
CC in the production of antibodies against them and in assays to identify
CC modulators of their expression and activity. The antibodies and
CC antagonists may also be used to down regulate expression and activity
CC and modulate angiogenesis. The antibodies may also be used as diagnostic
CC agents for detecting the presence of the polypeptides in samples.
CC Disorders that may be prevented, diagnosed and/or treated by the above
CC methods include, for example vascular tumours, proliferative tumours,
CC proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,
CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis
CC associated with neovascularisation, restenosis subsequent to balloon
CC angioplasty, scar tissue over production, peripheral vascular disease,
CC hypertension, inflammatory vasculitides, Reynaud's disease and
CC Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis,
CC lymphangitis, lymphedema, wound healing and tissue repair, ischaemia
CC reperfusion injury, angina, myocardial infarctions, chronic heart
CC conditions, heart failure such as congestive heart failure, age-related
CC macular degeneration and osteoporosis. AAH22255 to AAH23325 and AAB98322
CC to AAB98325 represent sequence used in the exemplification of the
CC present invention.
XX

SQ Sequence 19 BP; 1 A; 8 C; 6 G; 4 T; 0 other;

Query Match 1.8%; Score 19; DB 22; Length 19;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 978 ccgatgctgctccgcgct 996
|||||
DB 1 ccgatgctgctccgcgct 19

RESULT 30
AAK87821
ID AAK87821 standard; cDNA; 637 BP.

XX AAK87821;

XX 05-NOV-2001 (first entry)

DE Human digestive system antigen coding sequence SEQ ID NO: 137.

XX Human; digestive system antigen; gene therapy; cancer; appendicitis;
KM ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
KM digestive system disorder; Meckel's diverticulum; ss.

XX Homo sapiens.

XX WO200155314-A2.

PD 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01324.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.

PR 19-MAY-2000; 2000US-0205515.

PR 07-JUN-2000; 2000US-0209467.

PR 28-JUN-2000; 2000US-0214886.

PR 30-JUN-2000; 2000US-0215135.

XX Sequence 637 BP; 142 A; 193 C; 147 G; 150 T; 5 other;

Query Match 1.8%; Score 19; DB 22; Length 637;

Best Local Similarity 100.0%; Pred. No. 84;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 tgcctcctctgggacctgg 79

|||||

Db 362 tgcctcctctgggacctgg 380

Search completed: June 19, 2002, 02:21:30
Job time: 3821 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:16:19 ; Search time 47.29 Seconds
(without alignments)
5495.459 Million cell updates/sec

Title: US-09-852-845-1

Perfect score: 1058

Sequence: 1 cagcagagacagagatgtcgc.....cacatcaaaccttgccag 1058

Scoring table: OLIGO_NUC

Searched: 383533 seqs, 122816752 residues

Word size: 0

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :

Issued_Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A.COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B.COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A.COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B.COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCtus.COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	886	83.7	1057	US-08-147-784-1	Sequence 1, Appl
2	886	83.7	1057	US-08-195-967-1	Sequence 1, Appl
3	886	83.7	1057	US-08-472-940-1	Sequence 1, Appl
4	293	27.7	848	US-08-192-480A-1	Sequence 1, Appl
5	28	2.6	618	US-08-097-827-6	Sequence 6, Appl
6	28	2.6	618	US-08-494-574-6	Sequence 6, Appl
7	28	2.6	1317	US-08-097-827-10	Sequence 10, Appl
8	28	2.6	1317	US-08-494-574-10	Sequence 10, Appl
9	24	2.3	24	US-08-192-480A-2	Sequence 2, Appl
10	19	1.8	1413	US-08-984-709A-52	Sequence 52, Appl
11	19	1.8	7898	US-08-984-709A-49	Sequence 49, Appl
12	18	1.7	410	US-09-114-146-1	Sequence 1, Appl
13	18	1.7	410	PCT-US96-08623-1	Sequence 1, Appl
14	18	1.7	1645	US-08-934-386-1	Sequence 1, Appl
15	18	1.7	2344	US-08-893-852A-2	Sequence 2, Appl
16	18	1.7	2488	US-08-279-270A-2	Sequence 2, Appl
17	18	1.7	2550	US-08-188-228-53	Sequence 53, Appl
18	18	1.7	2550	US-08-332-643-47	Sequence 47, Appl
19	18	1.7	2550	US-08-332-638-53	Sequence 53, Appl
20	18	1.7	2647	US-08-136-118-3	Sequence 3, Appl
21	18	1.7	3147	US-08-781-802-7	Sequence 7, Appl
22	18	1.7	3147	US-08-694-078-7	Sequence 7, Appl
23	18	1.7	3243	US-09-058-260-7	Sequence 32, Appl
24	18	1.7	3243	US-08-611-107-32	Sequence 32, Appl
25	18	1.7	4157	US-08-162-146-2	Sequence 2, Appl
26	18	1.7	4157	US-09-314-127-2	Sequence 2, Appl
27	18	1.7	11748	US-08-611-107-30	Sequence 30, Appl

ALIGNMENTS

28	17	1.6	316	4	US-08-905-223-270	Sequence 270, App
29	17	1.6	507	4	US-08-894-818B-26	Sequence 26, Appl
30	17	1.6	545	2	US-08-583-562B-5	Sequence 5, Appl
31	17	1.6	545	2	US-08-778-113-5	Sequence 5, Appl
32	17	1.6	614	2	US-08-692-787-2	Sequence 2, Appl
33	17	1.6	614	4	US-09-097-199-2	Sequence 2, Appl
34	17	1.6	827	1	US-08-726-725-3	Sequence 3, Appl
35	17	1.6	1236	4	US-09-445-472-2	Sequence 2, Appl
36	17	1.6	1314	2	US-08-440-845D-9	Sequence 9, Appl
37	17	1.6	1314	2	US-08-868-458-9	Sequence 9, Appl
38	17	1.6	1509	2	US-08-791-347-2	Sequence 2, Appl
39	17	1.6	1512	2	US-08-645-900A-3	Sequence 3, Appl
40	17	1.6	1512	2	US-08-882-238A-3	Sequence 3, Appl
41	17	1.6	1512	2	US-08-667-790A-3	Sequence 3, Appl
42	17	1.6	1512	3	US-09-220-459-3	Sequence 3, Appl
43	17	1.6	1512	4	US-08-546-568B-3	Sequence 3, Appl
44	17	1.6	1512	4	US-08-822-999-2	Sequence 2, Appl
45	17	1.6	1548	4	US-08-938-669A-26	Sequence 26, Appl
46	17	1.6	1566	4	US-08-894-818B-4	Sequence 4, Appl
47	17	1.6	1670	3	US-08-709-838-1	Sequence 1, Appl
48	17	1.6	1670	4	US-08-829-839-1	Sequence 1, Appl
49	17	1.6	1962	4	US-08-894-818B-34	Sequence 34, Appl
50	17	1.6	1962	4	US-09-445-472-15	Sequence 15, Appl

RESULT 1
US-08-147-784-1
; Sequence 1, Application US/08147784
; Patent No. 5821332
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Buck, David
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend Kourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,784
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-220
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2420
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..845

OTHER INFORMATION: /standard_name= "ACT-4 CDNA"
US-08-147-784-1

Query Match	83.7%	Score 886;	DB 1;	Length 1057;
Best Local Similarity	99.8%	Pred. No. 0;		
Matches 1056; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1;

[illegible]

Db 960 CTGCACGTTCTAGCTGCCATGGCTGCGCTCTGCTTACGTATGCCATGCATTA 1019

0y 1021 cctctctgccccgcgagacacaaataaaaccttggag 1058

Db 1020 CCTCTCTGCCCCCGCGGACCAATATAAACCCTTGGCAG 1057

```

RESULT 2
US-08-195-967-1
Sequence 1, Application US/08195967
Patent No. 6242366
GENERAL INFORMATION:
APPLICANT: Godfrey, Wayne
APPLICANT: Engleman, Edgar G.
TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
TITLE OF INVENTION: CD4+ T-CELLS
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/195,967
FILING DATE: 10-FEB-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 05490A-230
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO.: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1057 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 15..845
OTHER INFORMATION: /standard_name= "ACT-4 cDNA"
US-08-195-967-1

```

[illegible]

Db	421	GGGCAACACAGGCGCTGCAAGCCTCTGGAGCCAACTGCACCTTGGCTGGGAAGACACACCTTGC	480
Qy	481	agcccgccagcaataagctctgtagcgcaactctgtgtagacagggaaaccccccagacagcagc	540
Db	481	AGCGCGGACAGCAATAAGCTCTGGAGCGCAATCTGTAGAGACAGGGACCCCCAGCACAGCGAGC	540
Qy	541	cccgaggagaccagagggcccccccgccagaggcccaactcaactctcagcccaactgaagcctgac	600
Db	541	CCGAGGAGACCCAGAGGCGCCCGCGGCGCAGGCGCATCTACTCTCCAGGCCCACTGAAGGCTTGC	600
Qy	601	ccagaacctcaagaggaaccttcaaccgcgcgttgtaggtctcccggggggcgtgacgttg	660
Db	601	CCAAACACTCACAGGGAGCCCTTCACCCCGGCGCCCTGAGAGGTCTCCCGGGGGCGCTGGCGTTG	660
Qy	661	ccggacatccctggagcctctggagcttggtctgtgaggtctgtgtggccccccttgccactctgtc	720
Db	661	CCGCGATCTCTGGGCTTGGGCTTGGGCTGTGTCTGTGGGCTGCTGGGCCCTTGGCATCTGCTGG	720
Qy	721	ccctgtacctgtctccgagaggagacaaaggctgcgcccccga1tgccacaagccccctggag	780
Db	721	CCCTGTACGTGCTCCGAGGAGACACAGGGGTGGCCCCCGATGCCACAAAGCCCCCTGGGG	780
Qy	781	gaggcaattcccggaacccccca1tccaaaggagagagcgagcgagccca1tccaeccctggcca	840
Db	781	GAGGCAATTTCCGAGACCCCATCATCAAGAGAGAGAGGCGCCAGCCCATCTCACCTGAGGCA	840
Qy	841	agaactgaaccttgagccccaagagctgtagcgtctgagcccccgcaagctgtagagccggag	900
Db	841	AGATCTGAC- TGGCGCCACACAAAGTGGAGACGTGGGCCCCGCGCAGAGCTGAGGCCGAGG	899
Qy	901	gtctgctggagcgagcaagagcagtgtagcagcgctgcgtcccgccagcgtctctggagccaact	960
Db	900	GTCGTCTGGGGGAGACAGGAGGAGGTGCAGGCGCGCTGCCCGGACAGCTCTGGGGCAACT	959
Qy	961	ctgagacgcttctatggtgcgaatgctgcgctcgcgtctctgtcttaagatgcatgcatca	1020
Db	960	CTGACCGGTTCTAGTGTCCGATGGCTGCTCCGGGCTCTCTGCTTACGTATGCAATGCAATA	1019
Qy	1021	ctctctgcccccgagagacacaataaaaccttgag	1058
Db	1020	CTCTCTGCCCCGGGAGCACCAATAAACAACCTTGGCAG	1057
RESULT 4			
US-08-192-480A-1			
: Sequence 1, Application US/08192480A			
: Patent No. 5759546			
: GENERAL INFORMATION:			
: APPLICANT: Andrew D. Weinberg and Arthur A.			
: APPLICANT: Vandenberg			
: TITLE OF INVENTION: TREATMENT OF CD4 T-CELL			
: TITLE OF INVENTION: MEDIATED CONDITIONS			
: NUMBER OF SEQUENCES: 3			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Richard J. Polley, Esq.			
: ADDRESSEE: Klarquist Sparkman Campbell			
: ADDRESSEE: Leigh & Whinston			
: STREET: 121 S.W. Salmon Street, Suite 1600			
: CITY: Portland			
: STATE: Oregon			
: COUNTRY: United States of America			
: ZIP: 97204			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Disk, 3-1/2 inch			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: MS DOS			
: SOFTWARE: WordPerfect 5.1			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/192,480A			
: FILING DATE:			
: CLASSIFICATION: 424			
: PRIOR APPLICATION DATA: N/A			
: APPLICATION NUMBER:			

```

1      FILING DATE:
2      ATTORNEY/AGENT INFORMATION:
3      NAME: Richard J. Polley, Esq.
4      REGISTRATION NUMBER: 28,107
5      REFERENCE/DOCKET NUMBER: 4282-38649
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: (503) 226-7391
8      TELEFAX: (503) 228-9446
9      INFORMATION FOR SEQ ID NO: 1:
10     SEQUENCE CHARACTERISTICS:
11     LENGTH: 848 base pairs
12     TYPE: Nucleic acid
13     STRANDEDNESS: Double
14     TOPOLOGY: Linear
15     MOLECULE TYPE: cDNA to mRNA
16     HYPOTHETICAL: NO
17     ANTI-SENSE: NO
18     FRAGMENT TYPE:
19     US-08-192-480A-1
20
21     Query Match      27.7%: Score 293; DB 1: Length 848;
22     Best Local Similarity 100.0%: Pred. NO. 1e-120; Mismatches 0; Indels 0; Gaps 0.
23     Matches 293: Conservative 0; Mismatches 0; Indels 0; Gaps 0.
24
25     QY      3      gcaagagacagagatgttgctgaggagctcgccgagctgggcccgggacgtgtgcgagctctg 62
26     Db      3      GCAGAGACGAGAGATGTGCTGGGGGGCTCGCGCGCTGGGCCCGGGCCGCTGCGGCTTG 62
27
28     QY      63      ctccctccctgggctgtgggcttgagcaccgttgacgggctcactgtgtcgggaaacctac 122
29     Db      63      CTCCTCTCGGGGCTTGGGGCTGAGCACCGGAGGGGGCTCTCACTGTGTGGGACACTAC 122
30
31     QY      123     cccaagcaacgacggtgtctgccaaggtgcaagccagggcaagggatgtgtgagccgctgc 182
32     Db      123     CCCACCAACGACGGGTGCTGCCACGATGTCAGAGCCACGCAACGGGATGTGTAGCCGCTGC 182
33
34     QY      183     agcgcgtccccaagaacacaggtgtgccgtccgctgcggggccggctcttaacaagaagtgtgc 242
35     Db      183     AGCCCCCTCCCAACACAGGTGTGCCGTCCGTCGGGGCCGGGCTTTCACCAACACAGCTGGTC 242
36
37     QY      243     agctccaagccgtgcaagccctgcacgctgtgttaacctcaagaagtggagtgta 295
38     Db      243     AGCTCAAGCCGTGCAAGCCCTGCACAGCTGTGTAACTTCAGAAAGTGGAGTGTA 295
39
40 RESULT 5
41 US-08-097-827-6
42 : Sequence 6, Application US/08097827
43 GENERAL INFORMATION:
44 APPLICANT: Baum, Peter
45             Goodman, Ray
46             Fanslow, William
47             Gayle, Richard
48 TITLE OF INVENTION: Novel Cytokine Which is a Ligand for OX40
49 NUMBER OF SEQUENCES: 13
50 CORRESPONDENCE ADDRESSES:
51 ADDRESSEE: Immunex Corporation
52 STREET: 51 University Street
53 CITY: Seattle
54 STATE: WA
55 COUNTRY: USA
56 ZIP: 98101
57 COMPUTER READABLE FORM:
58 MEDIUM TYPE: Floppy disk
59 COMPUTER: IBM PC compatible
60 OPERATING SYSTEM: PC-DOS/MS-DOS
61 SOFTWARE: PatentIn Release #1.0, Version #1.25
62 CURRENT APPLICATION DATA:
63 APPLICATION NUMBER: US/08/097,827
64 FILING DATE: 23-Jul-1993
65 CLASSIFICATION: <Unknown>
66

```

ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MOUSE OX40
FEATURE:
NAME/KEY: CDS
LOCATION: 1..618
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-097-827-6

Query Match 2.6%; Score 28; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 acaaccaggcctgcagccctggaccac 451
|||||
DB 404 ACAACGAGCCTGCAGCCCTGGACCAA 431

RESULT 6
US-08-494-574-6
Sequence 6, Application US/08494574
Patent No. 5783665
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine which is a ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 618 base pairs

TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MOUSE OX40
FEATURE:
NAME/KEY: CDS
LOCATION: 1..618
US-08-494-574-6

Query Match 2.6%; Score 28; DB 1; Length 618;
Best Local Similarity 100.0%; Pred. No. 0.0015;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 acaaccaggcctgcagccctggaccac 451
|||||
DB 404 ACAACGAGCCTGCAGCCCTGGACCAA 431

RESULT 7
US-08-097-827-10
Sequence 10, Application US/08097827
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: Novel Cytokine which is a ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MOX40Fc Mutein
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1317
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-08-097-827-10

Query Match 2.6%; Score 28; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 acaccaggcctgcgaagcctggaccac 451
|||||
DB 404 ACACACGCGCTGCAGCCCTGGACCAA 431

RESULT 8

US-08-494-574-10
; Sequence 10, Application US/08494574
; Patent No. 5783665

GENERAL INFORMATION:

APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine which is a ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574
FILING DATE: 22-JUN-1995
CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 1317 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: MOX40Fc Mutein
FEATURE:

NAME/KEY: CDS
; LOCATION: 1..1317
US-08-494-574-10

Query Match 2.6%; Score 28; DB 1; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 acaccaggcctgcgaagcctggaccac 451
|||||
DB 404 ACACACGCGCTGCAGCCCTGGACCAA 431

RESULT 9

US-08-192-480A-2
; Sequence 2, Application US/08192480A
; Patent No. 5759546

GENERAL INFORMATION:

APPLICANT: Andrew D. Weinberg and Arthur A.
APPLICANT: Vandenberg
TITLE OF INVENTION: TREATMENT OF CD4 T-CELL
TITLE OF INVENTION: MEDIATED CONDITIONS
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: Richard J. Polley, Esq.
ADDRESSEE: Klarquist Sparkman Campbell
ADDRESSEE: Leigh & Whinston
STREET: 121 S.W. Salmon Street, Suite 1600
CITY: Portland
STATE: Oregon
COUNTRY: United States of America

ZIP: 97204

COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/192,480A

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA: N/A

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Richard J. Polley, Esq.
REGISTRATION NUMBER: 28,107
REFERENCE/DOCKET NUMBER: 4282-38649
TELECOMMUNICATION INFORMATION:
TELEPHONE: (503) 226-7391
TELEFAX: (503) 228-9446

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 24 base pairs
TYPE: Nucleic acid
STRANDEDNESS: Single
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SENSE: NO

US-08-192-480A-2

Query Match 2.3%; Score 24; DB 1; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 atgtgcgtggggcctgcgcgctg 38
|||||
DB 1 ATGTGCGTGGGCGCTGCGCGCTG 24

RESULT 10

US-08-984-709A-52/C
; Sequence 52, Application US/08984709A
; Patent No. 6320032

GENERAL INFORMATION:

APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:

ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4250 Executive Square, Suite 700
CITY: La Jolla

STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 1413 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
US-08-984-709A-52

Query Match 1.8%; Score 19; DB 4; Length 1413;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 668 cctggcctgggacctggtg 686
|||||
Db 1313 cctggcctgggacctggtg 1295

RESULT 11
US-08-984-709A-49/c
Sequence 49, Application US/08984709A
Patent No. 6320032
GENERAL INFORMATION:
APPLICANT: Williams, Mark E.
APPLICANT: Stauderman, Kenneth A.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Heller Ehrman White & McCauliffe
STREET: 4250 Executive Square, Suite 700
CITY: La Jolla
STATE: California
COUNTRY: US
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/984,709A
FILING DATE: 02-DEC-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)

TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 450-8400
TELEFAX: (619) 587-5360
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 7898 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 249...7307
OTHER INFORMATION:
US-08-984-709A-49

Query Match 1.8%; Score 19; DB 4; Length 7898;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 668 cctggcctgggacctggtg 686
|||||
Db 2518 cctggcctgggacctggtg 2500

RESULT 12
US-09-114-146-1
Sequence 1, Application US/09114146
Patent No. 6083747
GENERAL INFORMATION:
APPLICANT: Wong, Peter M.C.
APPLICANT: CHUNG, Siu-Wah
APPLICANT: HAN, Xiaodong
TITLE OF INVENTION: GLYCOPROTEIN GPI05 ON BLS HEMATOPOIETIC
TITLE OF INVENTION: STEM CELLS
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/114,146
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/471,188
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 46074/102/FEIN
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
US-09-114-146-1

Query Match 1.7%: Score 18; DB 3; Length 410;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 tgcctgggagctgctggcc 702
|||||
DB 247 TCGTGGGCTGCTGGGCC 264

RESULT 13
PCT-US96-08623-1
; Sequence 1, Application PC/TUS9608623
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: GLYCOPROTEIN GP105 ON BLS HEMATOPOIETIC
; TITLE OF INVENTION: STEM CELLS
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/08623
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/471,188
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 46074/103/FEIN
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US96-08623-1

Query Match 1.7%: Score 18; DB 5; Length 410;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 685 tgcctgggagctgctggcc 702
|||||
DB 247 TCGTGGGCTGCTGGGCC 264

RESULT 14
US-08-934-386-1/c
; Sequence 1, Application US/08934386
; Patent No. 6306636
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; TITLE OF INVENTION: Methods for Detecting Nucleic Acid

TITLE OF INVENTION: Segments Encoding Acetyl-CoA Carboxylase
; NUMBER OF SEQUENCES: 68
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 433
; CITY: Houston
; STATE: Texas
; COUNTRY: US

ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/934,386
; FILING DATE: 19-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARSB:521
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1645 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-934-386-1

Query Match 1.7%: Score 18; DB 4; Length 1645;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 18: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 681 ctggctgctgggctgctg 698
|||||
DB 699 CTGGTCTGGGCTGCTGCTG 682

RESULT 15
US-08-893-852A-2/c
; Sequence 2, Application US/08893852A
; Patent No. 6080558
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Shah, Purvi
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW HUMAN GROWTH REGULATOR PROTEIN
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/893,852A
; FILING DATE: Filed Herewith
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0341 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2344 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: TML3DT01
CLONE: 508302
US-08-893-852A-2

Query Match 1.7%; Score 18; DB 3; Length 2344;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 gctcctcctggcctggg 79
|||||

Db 2032 GCTCCTCCTGGCCTGGG 2015

RESULT 16
US-08-279-270A-2
Sequence 2, Application US/08279270A
Patent No. 5691460
GENERAL INFORMATION:
APPLICANT: Duvic, Madeleine
TITLE OF INVENTION: Epidermal Surface Antigen and Uses
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/279, 270A
FILING DATE: Concurrently herewith
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfield, Denise L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTS#173--1/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/320-7200
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 2488 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-279-270A-2

Query Match 1.7%; Score 18; DB 1; Length 2488;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 669 ctgggcttggcctgtg 686
|||||

Db 72 CTGGGCTGGCCTGTG 89

RESULT 17
US-08-188-228-53/c
Sequence 53, Application US/08188228
Patent No. 5597725
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,228
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/049,460
FILING DATE: 19 APR 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5597725and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 2550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-188-228-53

Query Match 1.7%; Score 18; DB 1; Length 2550;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 663 gccatcctggcctgggc 680
|||||

Db 990 GCCATCCTGGCCTGGGC 973

RESULT 18
US-08-332-643-47/c
Sequence 47, Application US/08332643
Patent No. 5639634
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 56
CORRESPONDENCE ADDRESS:

ADDRESSER: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,643
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/872,643
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5639634and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 27866/30795
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 2550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-332-643-47

Query Match 1.7%; Score 18; DB 1; Length 2550;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 gccatcctggcctgggc 680
DB 990 gccatcctggcctgggc 973

RESULT 19
US-08-332-638-53/C
Sequence 53, Application US/08332638
Patent No. 5646250
GENERAL INFORMATION:
APPLICANT: Suzuki, Shintaro
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
STREET: 6300 Sears Tower, 233 S. Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,638
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643
FILING DATE: 17 APR 1992
APPLICATION NUMBER: US/08/049,460
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: No. 5646250and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31340
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 2550 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-332-638-53

Query Match 1.7%; Score 18; DB 1; Length 2550;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 gccatcctggcctgggc 680
DB 990 gccatcctggcctgggc 973

RESULT 20
US-08-136-119-3
Sequence 3, Application US/08136119
Patent No. 5473056
GENERAL INFORMATION:
APPLICANT: Helmbrook, David C.
APPLICANT: Hoyle, Mona I.
TITLE OF INVENTION: E2F-2, A NOVEL MAMMALIAN TRANSCRIPTION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Muthard
STREET: P.O. Box 2000, 126 Lincoln Avenue
CITY: Rahway
STATE: N.J.
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/136,119
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Muthard, David A.
REGISTRATION NUMBER: 35,297
REFERENCE/DOCKET NUMBER: 19042
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908)594-3903
TELEFAX: (908)594-4720
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2647 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-136-119-3

Query Match 1.7%; Score 18; DB 1; Length 2647;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 566 cagcccatcactgtcca 583
|||||
Db 2200 CAGGCCCATCACTGTCCA 2217

RESULT 21
US-08-781-802-7
; Sequence 7, Application US/08781802
; Patent No. 5969121
; GENERAL INFORMATION:
; APPLICANT: ALLEN, Larry
; APPLICANT: AIKENS, John
; APPLICANT: FONSTEIN, Michael
; APPLICANT: VONSTEIN, Veronika
; APPLICANT: DEMIRJIAN, David
; APPLICANT: CASADABAN, Malcolm
; TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 S. Wacker Drive 32nd Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,802
; FILING DATE: 10-JAN-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/694,078
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,580
; FILING DATE: 12-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/009,704
; FILING DATE: 11-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,995
; FILING DATE: 01-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 95,963-E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3147 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 245..1231
; OTHER INFORMATION: /note="Tspa E101 sequence longest
; OTHER INFORMATION: open reading frame; other possible start codons are TTG/Leu9;
; OTHER INFORMATION: TTG/Leu13; TTG/Leu15; GTG/Val43"

; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 245..1231
US-08-781-802-7

Query Match 1.7%; Score 18; DB 2; Length 3147;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 61 tgctcctcctggcctgg 78
|||||
Db 2214 TGCTCCTCCTGGGCGCTGG 2231

RESULT 22
US-08-694-078-7
; Sequence 7, Application US/08694078
; Patent No. 6218163
; GENERAL INFORMATION:
; APPLICANT: ALLEN, Larry
; APPLICANT: AIKENS, John
; APPLICANT: FONSTEIN, Michael
; APPLICANT: VONSTEIN, Veronika
; APPLICANT: DEMIRJIAN, David
; APPLICANT: CASADABAN, Malcolm
; TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff, Ltd.
; STREET: 300 S. Wacker Drive 7th Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/694,078
; FILING DATE: 07-AUG-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/019,580
; FILING DATE: 12-JUN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/009,704
; FILING DATE: 10-JAN-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/001,995
; FILING DATE: 07-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Chao, Mark
; REGISTRATION NUMBER: 37,293
; REFERENCE/DOCKET NUMBER: 95,963-C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-913-0001
; TELEFAX: 312-913-0002
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3147 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 245..1231
; OTHER INFORMATION: /note="Tspa E101 sequence longest
; OTHER INFORMATION: open reading frame; other possible start codons are TTG/Le
; OTHER INFORMATION: TTG/Leu13; TTG/Leu15; GTG/Val43"

```

; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 245..1231
US-08-694-078-7

Query Match      1.7%; Score 18; DB 4; Length 3147;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 61 tgcctcctcctggcctg 78
   |||
Db 2214 tgcctcctcctggcctg 2231

RESULT 23
US-09-058-260-7
; Sequence 7, Application US/09058260B
; Patent No. 6218167
; GENERAL INFORMATION:
; APPLICANT: Allen, Larry
; APPLICANT: Alkens, John
; APPLICANT: Fousteln, Michael
; APPLICANT: Vonsteijn, Veronika
; APPLICANT: Demirjian, David
; APPLICANT: Casadaban, Malcolm
; TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis
; FILE REFERENCE: 95-963-H
; CURRENT APPLICATION NUMBER: US/09/058,260B
; EARLIER FILING DATE: 1999-04-10
; EARLIER APPLICATION NUMBER: 60/001,995
; EARLIER FILING DATE: 1996-08-07
; EARLIER APPLICATION NUMBER: 60/009,704
; EARLIER FILING DATE: 1996-01-11
; EARLIER APPLICATION NUMBER: 60/019,580
; EARLIER FILING DATE: 1996-06-12
; EARLIER APPLICATION NUMBER: 08/694,078
; EARLIER FILING DATE: 1996-08-08
; EARLIER APPLICATION NUMBER: 08/781,802
; EARLIER FILING DATE: 1997-01-10
; EARLIER APPLICATION NUMBER: 08/827,810
; EARLIER FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 3147
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:cloned esterase
; OTHER INFORMATION: gene from bacteria E101
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (245)..(1231)
US-09-058-260-7

Query Match      1.7%; Score 18; DB 4; Length 3147;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 61 tgcctcctcctggcctg 78
   |||
Db 2214 tgcctcctcctggcctg 2231

RESULT 24
US-08-611-107-32/C
; Sequence 32, Application US/08611107
; Patent No. 5801233
; GENERAL INFORMATION:
; APPLICANT: Haselkorn, Robert
; APPLICANT: Gornicki, Piotr
; APPLICANT: Gornicki, Piotr
```

```

; TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
; TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USBS
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 40
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: United States of America
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/611,107
; FILING DATE: Concurrently Herewith
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 07/956,700
; FILING DATE: 02-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US PCT/US93/09340
; FILING DATE: 30-SEP-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US SN 08/422,560
; FILING DATE: 14-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: ARCD:221
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (512) 474-7577
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-611-107-32

Query Match      1.7%; Score 18; DB 1; Length 3243;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 681 ctggtgctgggctgctg 698
   |||
Db 2300 ctggtgctgggctgctg 2283

RESULT 25
US-08-162-146-2/C
; Sequence 2, Application US/08162146
; Patent No. 5965788
; GENERAL INFORMATION:
; APPLICANT: HOUEBERNE, Louis-Marie
; APPLICANT: DEVINOY, Eve
; APPLICANT: THEPOT, Dominique
; TITLE OF INVENTION: Production of a Protein of Interest in
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/162,146
FILING DATE: 10-FEB-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00533
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/07179
FILING DATE: 12-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1868..1949, 2462..2587, 2888..3046, 3416
LOCATION: ..3429)
US-08-162-146-2

Query Match 1.7%; Score 18; DB 2; Length 4157;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 667 tcctggcctggcctgg 684
|||||
Db 901 tcctggcctggcctgg 884

RESULT 26
US-09-314-127-2/c
Sequence 2, Application US/09314127
Patent No. 6268545
GENERAL INFORMATION:
APPLICANT: HOUDEBINE, Louis-Marie
APPLICANT: DEVINOV, Eve
APPLICANT: THEPOT, Dominique
TITLE OF INVENTION: Production of a Protein of Interest in
TITLE OF INVENTION: the Milk of a Transgenic Mammalian
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/314,127
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,146
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91/07179
FILING DATE: 12-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: WEGNER, Harold C.
REGISTRATION NUMBER: 25,258
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 4157 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1868..1949, 2462..2587, 2888..3046, 3416
LOCATION: ..3429)
US-09-314-127-2

Query Match 1.7%; Score 18; DB 4; Length 4157;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 667 tcctggcctggcctgg 684
|||||
Db 901 tcctggcctggcctgg 884

RESULT 27
US-08-611-107-30/c
Sequence 30, Application US/08611107
Patent No. 5801233
GENERAL INFORMATION:
APPLICANT: Haselkorn, Robert
APPLICANT: Gornickl, Piotr
TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE AND USBS
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P O Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,107
FILING DATE: Concurrently Herewith
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 07/956,700
FILING DATE: 02-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US PCT/US93/09340
FILING DATE: 30-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US SN 08/422,560
FILING DATE: 14-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: ARCD:221
TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 11748 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-611-107-30

Query Match 1.7%; Score 18; DB 1; Length 11748;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 681 ctgctgctg9g9gctgctg 698
|||||
DB 89 CTGCTGCTGGGCTGCTG 72

RESULT 28

US-08-905-223-270
Sequence 270, Application US/08905223
Patent No. 6222029

GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Duclert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92101-3505

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95

SOFTWARE: Word

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223

FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Israelien, Ned A.
REGISTRATION NUMBER: 29,655

REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550

TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 270:

SEQUENCE CHARACTERISTICS:

LENGTH: 316 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: DOUBLE

TOPOLOGY: LINEAR

MOLECULE TYPE: CDNA

ORIGINAL SOURCE:

ORGANISM: Homo Sapiens

TISSUE TYPE: Brain

FEATURE:

NAME/KEY: other

LOCATION: 212..311

IDENTIFICATION METHOD: fasta

OTHER INFORMATION: Identity 93

OTHER INFORMATION: region 1..101

OTHER INFORMATION: Id HSSCOASN

OTHER INFORMATION: vrt

FEATURE:

NAME/KEY: other

LOCATION: 243..311
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: Identity 94
OTHER INFORMATION: region 60..128
OTHER INFORMATION: Id AA135265
OTHER INFORMATION: est

FEATURE:
NAME/KEY: other
LOCATION: 187..245
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: Identity 91
OTHER INFORMATION: region 3..63
OTHER INFORMATION: Id AA135265
OTHER INFORMATION: est

FEATURE:
NAME/KEY: other
LOCATION: 269..311
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: Identity 100
OTHER INFORMATION: region 49..91
OTHER INFORMATION: Id R58602
OTHER INFORMATION: est

FEATURE:
NAME/KEY: sig_peptide
LOCATION: 179..250
IDENTIFICATION METHOD: Von Heljne matrix
OTHER INFORMATION: score 4.8
OTHER INFORMATION: seq ATWVGSSGLAXA/RL
US-08-905-223-270

Query Match 1.6%; Score 17; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 ggaagtcgccg9g9gccc 651
|||||
DB 144 GGAGTCCCGGGGGCC 160

RESULT 29

US-08-894-818B-26
Sequence 26, Application US/08894818B
Patent No. 6261822

GENERAL INFORMATION:

APPLICANT: TAKAKURA, Hikaru

APPLICANT: MORISHITA, Mio

APPLICANT: YAMAMOTO, Katsuhiko

APPLICANT: MITTA, Masanori

APPLICANT: ASADA, Kiyozo

APPLICANT: TSUNASAWA, Susumu

APPLICANT: KATO, Ikunoshin

TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES

NUMBER OF SEQUENCES: 42

CORRESPONDENCE ADDRESS:

ADDRESSEE: Broadway and Neimark

STREET: 419 Seventh Street N.W., Ste. 300

CITY: Washington

STATE: D.C.

COUNTRY: United States of America

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,818B

FILING DATE: 20-MAY-1998

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/JP96/03253

FILING DATE: 07-NOV-1996

PRIOR APPLICATION DATA:
: APPLICATION NUMBER: JP 323285/1995
: FILING DATE: 12-DEC-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Browdy, Roger L.
: REGISTRATION NUMBER: 25,618
: REFERENCE/DOCKET NUMBER: TAKAKURA-1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 628-5197
: TELEFAX: (202) 737-3528
: INFORMATION FOR SEQ ID NO: 26:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 507 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: genomic DNA
: US-08-894-818B-26

Query Match 1.6%; Score 17; DB 4; Length 507;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 968 gtctaggtgccgatg 984
|||||
Db 383 GTCTAGGTGCCGATG 399

RESULT 30
US-08-583-562B-5
: Sequence 5, Application US/08583562B
: Patent No. 5922570
: GENERAL INFORMATION:
: APPLICANT: Staunton, Donald
: APPLICANT: Harris, Edith
: TITLE OF INVENTION: Cytoplasmic Modulators of Integrin
: TITLE OF INVENTION: Binding
: NUMBER OF SEQUENCES: 36
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 233 South Wacker Drive, 6300 Sears Tower
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/583,562B
: FILING DATE:
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Williams Jr., Joseph A.
: REGISTRATION NUMBER: 38,659
: REFERENCE/DOCKET NUMBER: 27866/33033
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: INFORMATION FOR SEQ ID NO: 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 545 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..534
: US-08-583-562B-5

Query Match 1.6%; Score 17; DB 2; Length 545;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 71 gggcctgggctgaagca 87
|||||
Db 279 GGGCCTGGGCTGAGCA 295

Search completed: June 19, 2002, 02:17:34
Job time: 3675 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:26:22 ; Search time 17.65 Seconds
(without alignments)
1508.031 Million cell updates/sec

Title: US-09-852-845-2
Perfect score: 277
Sequence: 1 MCVGARRLGRGPCAALLLLG.....SFRPTIOEQADAHSTLAKI 277

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277	100.0	277	2 I37552	OX40 homolog - hum
2	272	4.3	271	2 S12783	gene OX40 antigen precu
3	12	4.3	272	2 I48700	hypothetical prote
4	8	2.9	78	2 F28771	hypothetical prote
5	8	2.9	122	2 S56343	hypothetical prote
6	8	2.9	151	2 T43478	hypothetical prote
7	8	2.9	162	2 E70195	colicin V producti
8	8	2.9	215	2 T22446	hypothetical prote
9	8	2.9	236	2 I51740	MHC class II alpha
10	8	2.9	236	2 I51741	MHC class II alpha
11	8	2.9	250	2 JH0749	class II histocomp
12	8	2.9	315	2 H89888	conserved hypothet
13	8	2.9	329	2 S31580	storage protein, b
14	8	2.9	329	2 S17765	major storage prot
15	8	2.9	394	2 C36942	hypothetical prote
16	8	2.9	443	2 D83106	hypothetical prote
17	8	2.9	445	2 B65221	probable amino aci
18	8	2.9	445	2 A91266	probable amino aci
19	8	2.9	445	2 F86106	probable amino aci
20	8	2.9	445	2 AF1032	probable amino aci
21	8	2.9	473	2 G70607	probable amino aci
22	8	2.9	476	2 E87040	acyl-CoA synthase
23	8	2.9	513	2 A95154	sodium/solute sym
24	8	2.9	575	2 D69611	ABC transporter re
25	8	2.9	578	2 A35810	alpha, alpha-trehal
26	8	2.9	583	2 JG6504	alpha, alpha-trehal
27	8	2.9	768	2 T00073	hypothetical prote
28	8	2.9	1031	2 T06130	hypothetical prote
29	7	2.5	52	2 T01742	hypothetical prote

30	7	2.5	88	2 T08512	trbo protein - Ent
31	7	2.5	91	2 B71391	NMDH dehydrogenase
32	7	2.5	93	2 C75603	hypothetical prote
33	7	2.5	96	2 A32954	gro-alpha precursor
34	7	2.5	101	2 B64997	hypothetical prote
35	7	2.5	101	2 B91023	hypothetical prote
36	7	2.5	101	2 C85867	hypothetical prote
37	7	2.5	101	2 AB0506	probable transcrip
38	7	2.5	103	2 D75449	suge protein - Del
39	7	2.5	103	2 AF0795	conserved hypothet
40	7	2.5	116	2 C72232	hypothetical prote
41	7	2.5	119	1 HSD01B	histone H1b, sperm
42	7	2.5	131	2 PQ0059	T-cell receptor be
43	7	2.5	133	2 S76950	hypothetical prote
44	7	2.5	139	2 A81938	probable membrane
45	7	2.5	142	2 AG1555	hypothetical prote
46	7	2.5	142	2 A11197	hypothetical prote
47	7	2.5	149	2 AH0505	probable membrane
48	7	2.5	152	2 A82182	hypothetical prote
49	7	2.5	155	2 F83341	hypothetical prote
50	7	2.5	156	2 AD1175	hypothetical prote

ALIGNMENTS

RESULT	1	
I37552	OX40 homolog - human	
C:Species: Homo sapiens (man)		
C:Date: 29-May-1998	#sequence_revision 29-May-1998	#text_change 11-Jan-2000
C:Accession: I37552		
R:Latza, U.; Durkop, H.; Schnitger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo		
Eur. J. Immunol. 24, 677-683, 1994		
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen		
A:Reference number: I37552; MUID:94170844		
A:Accession: I37552		
A>Status: preliminary; translated from GR/EMBL/DBJ		
A:Molecule type: mRNA		
A:Residues: 1-277 <RES>		
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CA53576.1; PID:9472958		
C:Superfamily: CD27 antigen; NCF receptor repeat homology		
Query Match	100.0%; Score 277; DB 2; Length 277;	
Best Local Similarity	100.0%; Pred. No. 2.5e-260;	
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
OY	1 MCVGARRLGRGPCAALLLLGLGLSTVTGLHCYGDYPSNDRCHRCRPGNGVNSRCSRSQ 60	
DB	1 MCVGARRLGRGPCAALLLLGLGLSTVTGLHCYGDYPSNDRCHRCRPGNGVNSRCSRSQ 60	
OY	61 NTVCRRPGGPFYNDVSSKPKCKPTWCNLRSGSERKKQLCTATQDTVCRCRAGTQPLDSYK 120	
DB	61 NTVCRRPGGPFYNDVSSKPKCKPTWCNLRSGSERKKQLCTATQDTVCRCRAGTQPLDSYK 120	
OY	121 PGVDCAPCPGPHFSRSDNACKPMWNTCTLACGHTLQPSNSSDAICEDRDPATQPOETQ 180	
DB	121 PGVDCAPCPGPHFSRSDNACKPMWNTCTLACGHTLQPSNSSDAICEDRDPATQPOETQ 180	
OY	181 GPPARPITVQPEAMPRTSOGSPTRPVEVPGGRAVAAILGLVLGILGPIAIIATLVLL 240	
DB	181 GPPARPITVQPEAMPRTSOGSPTRPVEVPGGRAVAAILGLVLGILGPIAIIATLVLL 240	
OY	241 RRDQRLPPDAHKPPGGSFRTPIOEQADAHSTLAKI 277	
DB	241 RRDQRLPPDAHKPPGGSFRTPIOEQADAHSTLAKI 277	
RESULT	2	
S12783	OX40 antigen precursor - rat	
N:Alternate names: nerve growth factor receptor homolog		

```

C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Maletty, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A:Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A:Reference number: S12783; MUID:90214614
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TMW>

Query Match 4.3%; Score 12; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149
|||||
DB 135 NOACKPWTNCTL 146

RESULT 3
148700
gene ox40 protein - mouse
N:Alternate names: OX40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Bullmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell int
A:Reference number: I48700; MUID:94044750
A:Accession: I48700
A:Molecule type: mRNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:9312827; PIDN:CAA79772.1; PID:9312828
R:Bireland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A:Reference number: I48334; MUID:95255413
A:Accession: I48334
A:Molecule type: DNA
A:Status: translated from GB/EMBL/DBJ
A:Residues: 1-14, 'G', 16-272 <RES>
A:Cross-references: EMBL:X85214; NID:9732818; PIDN:CAA59476.1; PID:9732819
C:Genetics:
A:Gene: OX40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 4.3%; Score 12; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149
|||||
DB 136 NOACKPWTNCTL 147

RESULT 4
F28771
hypothetical protein C397 (photosynthetic gene cluster) - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Jun-1993
C:Accession: F28771

```

```

R:Yovan, D.C.; Bylina, E.J.; Alberti, M.; Begusch, H.; Hearst, J.E.
Cell 37, 949-957, 1984
A:Title: Nucleotide and deduced polypeptide sequences of the photosynthetic reaction-
A:Reference number: A90850; MUID:84259352
A:Accession: F28771
A:Molecule type: DNA
A:Residues: 1-78 <YOV>
A:Cross-references: GB:K01183

Query Match 2.9%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LGLGLVVG 226
|||||
DB 39 LGLGLVVG 46

RESULT 5
S56343
hypothetical protein f122 - Escherichia coli
C:Species: Escherichia coli
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C:Accession: S56343
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from
A:Reference number: S56314; MUID:95334362
A:Accession: S56343
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-122 <BUR>
A:Cross-references: EMBL:U14003; NID:91263172; PIDN:AAA97014.1; PID:9536959
C:Genetics:
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A:start codon: GTG

Query Match 2.9%; Score 8; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CAALLLLG 20
|||||
DB 46 CAALLLLG 53

RESULT 6
T43478
hypothetical protein DKFZp434N1535.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z22516
A:Accession: T43478
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-151 <AAA>
A:Cross-references: EMBL:AL133575
A:Experimental source: adult testis; clone DKFZp434N1535
C:Genetics:
A:Note: DKFZp434N1535.1

Query Match 2.9%; Score 8; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 LGLSTVVG 28
|||||

```

Db 35 LGLSTVWG 42

RESULT 7

E70195

collin V production protein homolog - Lyme disease spirochete

C:Species: Borrelia burgdorferi (Lyme disease spirochete)

C>Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C:Accession: E70195

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lahlhira, R.; White son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.

A:Reference number: A70100; MUID:98065943

A:Accession: E70195

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-162 <KLE>

A:Cross-references: GB:AE001176; GB:AE000783; NID:g2688699; PIDN:AC67114.1; PID:g268870

A:Experimental source: strain B31

Query Match 2.9%; Score 8; DB 2; Length 162;

Best Local Similarity 100.0%; Pred. No. 6.2;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 LGLVLGL 228

Db 107 LGLVLGL 114

RESULT 8

T22446

hypothetical protein F49E12.7 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T22446

R:Thomas, K.

Submitted to the EMBL Data Library, October 1995

A:Reference number: Z19565

A:Accession: T22446

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-215 <WIL>

A:Cross-references: EMBL:Z66520; PIDN:CAA91386.1; GSPDB:GND0020; CESP:F49E12.7

A:Experimental source: clone F49E12

C:Genetics:

A:Gene: CESP:F49E12.7

A:Map position: 2

A:Introns: 44/3; 69/3; 136/1

Query Match 2.9%; Score 8; DB 2; Length 215;

Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 PLAILAL 237

Db 25 PLAILAL 32

RESULT 9

I51740

MHC class II alpha chain - zebra fish

C:Species: Brachydanio rerio (zebra fish)

C>Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 20-Sep-1999

C:Accession: I51740

R:Sultmann, H.; Meyer, W.E.; Figueroa, F.; O'Huigin, C.; Klein, J.

Immunogenetics 38, 408-420, 1993

A>Title: Zebrafish MHC class II alpha chain-encoding genes: polymorphism, expression, an

A:Reference number: I51740; MUID:94011091

A:Accession: I51740

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-236 <SUL>

A:Cross-references: GB:L19445; NID:g311192; PID:g311193

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 2.9%; Score 8; DB 2; Length 236;

Best Local Similarity 100.0%; Pred. No. 8.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVLGLG 229

Db 214 GLVLGLG 221

RESULT 10

I51741

MHC class II alpha chain - zebra fish

C:Species: Brachydanio rerio (zebra fish)

C>Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 20-Sep-1999

C:Accession: I51741; I51745

R:Sultmann, H.; Meyer, W.E.; Figueroa, F.; O'Huigin, C.; Klein, J.

Immunogenetics 38, 408-420, 1993

A>Title: Zebrafish MHC class II alpha chain-encoding genes: polymorphism, expression,

A:Reference number: I51740; MUID:94011091

A:Accession: I51741

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-236 <SUL>

A:Cross-references: GB:L19446; NID:g311194; PID:g311195

A:Accession: I51745

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-236 <SUL>

A:Cross-references: GB:L19450; NID:g311202; PID:g311203

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 2.9%; Score 8; DB 2; Length 236;

Best Local Similarity 100.0%; Pred. No. 8.4;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVLGLG 229

Db 214 GLVLGLG 221

RESULT 11

JH0749

class II histocompatibility antigen H-20 alpha chain precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 21-Jan-2000

C:Accession: JH0749

R:Karlsson, L.; Peterson, P.A.

J Exp. Med. 176, 477-483, 1992

A>Title: The alpha chain gene of H-20 has an unexpected location in the major histoco

A:Reference number: JH0749; MUID:92364550

A:Accession: JH0749

A:Molecule type: mRNA

A:Residues: 1-250 <KAR>

A:Cross-references: GB:M95514; NID:g199312; PIDN:AAB46387.1; PID:g199313

A:Experimental source: splenocyte

C:Genetics:

A:Introns: 28/1; 111/1; 205/1; 250/2

C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

C:Keywords: glycoprotein; heterodimer; transmembrane protein

F:1-25/Domain: signal sequence #status predicted <SIG>

F:26-250/Product: class II histocompatibility antigen H-20 alpha chain #status predic

F:126-191/Domain: immunoglobulin homology <IMM>

F:219-240/Domain: transmembrane #status predicted <TM>

F:104,144/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 2.9%; Score 8; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 GGLVGL 227
DB 222 GGLVGL 229
|||||

RESULT 12
H89888
Conserved hypothetical protein SA1016 [Imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89888
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.;
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <KUR>
A:Cross-references: GB:BA000018; PID:g13700972; PIDN:BAB42268.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1016

Query Match 2.9%; Score 8; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 GVLGLG 229
DB 12 GVLGLG 19
|||||

RESULT 13
S31580
Storage protein, bark - cottonwood
C:Species: Populus deltoides (cottonwood)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C:Accession: S31580
R:Coleman, G.D.; Chen, T.H.H.
Submitted to the EMBL Data Library, December 1992
A:Reference number: S31580
A:Accession: S31580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-329 <COL>
A:Cross-references: EMBL:X70064; NID:g20464; PID:g20465
C:Genetics:
A:introns: 102/1; 153/1; 216/1; 274/2

Query Match 2.9%; Score 8; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLGL 21
DB 7 AALLLGL 14
|||||

RESULT 14
S17765
Major storage protein - Carolina poplar
C:Species: Populus x canadensis (Carolina poplar)

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Sep-1997
C:Accession: S17765; S25320
R:Clausen, S.; Apel, K.
Plant Mol. Biol. 17, 669-678, 1991
A:Title: Seasonal changes in the concentration of the major storage protein and its m
A:Reference number: S17765; MUID:92003681
A:Accession: S17765
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-329 <CLA>
A:Cross-references: GB:S59422; NID:9237632; PID:9237633
A:Note: the authors translated the codon CNG for residues 15 and 16 as Leu, TTT for r
R:Clausen, S.; Apel, K.
Plant Mol. Biol. 20, 365, 1992
A:Title: Seasonal changes in the concentration of the major storage protein and its m
A:Reference number: S25320; MUID:93004495
A:Accession: S25320
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 15-19 <CL2>

Query Match 2.9%; Score 8; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLGL 21
DB 7 AALLLGL 14
|||||

RESULT 15
C36942
Hypothetical protein PA4219 [Imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 06-Oct-2000
C:Accession: C36942; G83119
R:Ankenbauer, R.G.; Quan, H.N.
J. Bacteriol. 176, 307-319, 1994
A:Title: FpA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate
A:Reference number: A36942; MUID:94117363
A:Accession: C36942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <ANK>
A:Cross-references: GB:U03161; NID:9454352; PIDN:AAQ3215.1; PID:9454355
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; L
.. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: G83119
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <STO>
A:Cross-references: GB:AE004638; GB:AE004091; NID:9950422; PIDN:AAQ7607.1; GSPDB:GN
C:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4219
C:Superfamily: Pseudomonas aeruginosa hypothetical protein (fpta 3' region)

Query Match 2.9%; Score 8; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLGL 21
DB 280 AALLLGL 287
|||||

RESULT 16
D83106
hypothetical protein PA4323 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83106
R:Stover, C.K.; Plam, X.O.; Eryin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardi, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
gen
A:Reference number: A82950; MUID:20437337
A:Accession: D83106
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-443 <STO>
A:Cross-references: GB:AE004848; GB:AE004091; NID:g9950537; PIDN:AG07711.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4323

Query Match 2.9%; Score 8; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 14 CAALLLGL 21
|||||||
DB 44 AALLLGL 51

RESULT 17
B65221
probable amino acid/amine transport protein [similarity] - Escherichia coli (strain K-12
N:Alternate names: hypothetical protein f326a
C:Species: Escherichia coli
C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Nov-2001
C:Accession: B65221; S56344
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Ce
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617
A:Accession: B65221
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-445 <BLAT>
A:Cross-references: GB:AE000484; GB:U00096; NID:g2367352; PIDN:AAC77076.1; PID:g2367353;
A:Experimental source: strain K-12, substrain MG1655
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.
A:Reference number: S56314; MUID:95334362
A:Accession: S56344
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-321, 'SOMR', 326 <BUR>
A:Cross-references: EMBL:U14003; NID:g1263172; PIDN:AA97015.1; PID:g536960
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
C:Superfamily: L-lysine transport protein

Query Match 2.9%; Score 8; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CAALLLGL 20
|||||||
DB 369 CAALLLGL 376

RESULT 18
A91266

probable amino acid/amine transport protein ECs5097 [imported] - Escherichia coli (st
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: A91266
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g
A:Reference number: A99629; MUID:21156231; PMID:11258796
A:Accession: A91266
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA838520.1; PID:g13364574; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain R1MD 0509952
C:Genetics:
A:Gene: ECs5097
C:Superfamily: L-lysine transport protein

Query Match 2.9%; Score 8; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 13 CAALLLGL 20
|||||||
DB 369 CAALLLGL 376

RESULT 19
F86106
probable amino acid/amine transport protein [similarity] - Escherichia coli (strain O
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 02-Nov-2001
C:Accession: F86106
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Diallanta, E.; Potamouisis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: F86106
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-445 <STO>
A:Cross-references: GB:AE005174; NID:g12519085; PIDN:AG59314.1; GSPDB:GN00145; UMGF:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yjde
C:Superfamily: L-lysine transport protein

Query Match 2.9%; Score 8; DB 2; Length 445;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CAALLLGL 20
|||||||
DB 369 CAALLLGL 376

RESULT 20
AF1022
probable amino acid permease SRY4493 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: This species has also been called Salmonella typhi
C>Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C:Accession: AF1022
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Church
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr
S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A:Reference number: AB0502; PMID:11677608
 A:Accession: AF1022
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-445 <PAR>
 A:Cross-references: GB:AL513382; PIDN:CAM09279.1; PID:g16505283; GSPDB:GN00176
 C:Genetics:
 A:Gene: STR4493
 C:Superfamily: L-lysine transport protein

Query Match 2.9%; Score 8; DB 2; Length 445;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CAAALLLG 20
 |||||
 Db 369 CAAALLLG 376

RESULT 21
 G70607
 probable fadD36 protein - Mycobacterium tuberculosis (strain H37RV)
 C:Species: Mycobacterium tuberculosis
 C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
 C:Accession: G70607
 R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
 Nature 393, 537-544, 1998
 A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
 A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
 A:Reference number: A70500; MUID:98293987
 A:Accession: G70607
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-473 <COL>
 A:Cross-references: GB:Z93777; GB:AL123456; NID:93261726; PIDN:CAM07836.1; PID:g1929067
 A:Experimental source: strain H37RV
 C:Genetics:
 A:Gene: fadD36
 C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology
 F:42-469/Domain: acetate--CoA ligase homology <AC1>

Query Match 2.9%; Score 8; DB 2; Length 473;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVLGLLG 229
 |||||
 Db 184 GLVLGLLG 191

RESULT 22
 E87040
 acyl-CoA synthase [imported] - Mycobacterium leprae
 C:Species: Mycobacterium leprae
 C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 15-Jun-2001
 C:Accession: E87040
 R:Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HC
 R.; Davies, R.M.; Devlin, K.; Dutthoy, S.; Feldwell, T.; Fraser, A.; Hamlin, N.; Holroyd,
 eam, M.A.; Rutherford, K.M.
 Nature 409, 1007-1011, 2001
 A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq
 A:Title: Massive gene decay in the leprosy bacillus.
 A:Reference number: A86909; MUID:21128732; PMID:11234002
 A:Accession: E87040
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-476 <STO>
 A:Cross-references: GB:AL450380; NID:g13093059; PIDN:CAC31432.1; GSPDB:GN00147
 C:Genetics:

A:Gene: xclC
 C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

Query Match 2.9%; Score 8; DB 2; Length 476;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVLGLLG 229
 |||||
 Db 187 GLVLGLLG 194

RESULT 23
 A95154
 sodium/solute symporter family protein [imported] - Streptococcus pneumoniae (strain
 C:Species: Streptococcus pneumoniae
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001
 C:Accession: A95154
 R:Retelien, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H
 on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzappel
 nson, T.; Hickey, E.K.; Holt, I.E.
 Science 293, 498-506, 2001
 A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris
 A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.
 A:Reference number: A95000; MUID:21357209; PMID:11463916
 A:Accession: A95154
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-513 <KUR>
 A:Cross-references: GB:AE005672; PIDN:AAK75426.1; PID:g14972810; GSPDB:GN00164; TIGR:
 A:Experimental source: strain TIGR4
 C:Genetics:
 A:Gene: SPI328

Query Match 2.9%; Score 8; DB 2; Length 513;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVLGLLG 229
 |||||
 Db 414 GLVLGLLG 421

RESULT 24
 D69611
 ABC transporter required for expression of cytochrome bd (ATP-) cydD - Bacillus subtil
 C:Species: Bacillus subtilis
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 02-Feb-2001
 C:Accession: D69611
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gal
 tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M
 Koeltter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lardino
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma
 Y, M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl
 A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowaka, A.; Se
 skeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya
 T.; Whitters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtili
 A:Reference number: A65980; MUID:98044033
 A:Accession: D69611
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-575 <KUN>
 A:Cross-references: GB:Z99123; GB:AL009126; NID:92636240; PIDN:CAB15899.1; PID:el1863
 A:Experimental source: strain 168

C:Genetics:
A:Gene: cydD
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology
C:Keywords: ATP; nucleotide binding; P-loop
F:353-356/Domain: ATP-binding cassette homology <ABC>
F:370-377/Region: nucleotide-binding motif A (P-loop)

Query Match 2.9%; Score 8; DB 2; Length 575;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 232 AALLALYL 239
|||||
DB 160 AALLALYL 167

RESULT 25
A35810
alpha,alpha-trehalase (EC 3.2.1.28) precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 23-Oct-1990 #sequence_revision 23-Oct-1990 #text_change 02-Jun-2000
C:Accession: A35810
R:Rut, J.; Wacker, H.; James, P.; Maffia, M.; Seiler, P.; Galand, G.; von Kieckebusch, A.
J. Biol. Chem. 265, 15034-15039, 1990
A:Title: Rabbit small intestinal trehalase. Purification, cDNA cloning, expression, and
A:Reference number: A35810; MUID:90368681
A:Accession: A35810
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-578 <RUF>
A:Cross-references: GB:M55299; NID:g164736; PIDN:AAA63460.1; PID:g164737; GB:M6523
C:Superfamily: human alpha,alpha-trehalase
C:Keywords: glycosidase; hydrolase

Query Match 2.9%; Score 8; DB 2; Length 578;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLGIGL 23
|||||
DB 11 LLLLGIGL 18

RESULT 26
JC6504
alpha,alpha-trehalase (EC 3.2.1.28) - human
C:Species: Homo sapiens (man)
C>Date: 04-Sep-1998 #sequence_revision 04-Sep-1998 #text_change 20-Jun-2000
C:Accession: JC6504
R:Ishihara, R.; Taketani, S.; Sasaki-Takedatsu, M.; Kino, M.; Tokunaga, R.; Kobayashi, Y.
Gene 202, 63-74, 1997
A:Title: Molecular cloning, sequencing and expression of cDNA encoding human trehalase.
A:Reference number: JC6504; MUID:98087419
A:Accession: JC6504
A:Molecule type: mRNA
A:Status: preliminary
A:Residues: 1-583 <ISH>
A:Cross-references: DDBJ:AB000824; NID:g2789460; PIDN:BAA2381.1; PID:g2789461
C:Superfamily: human alpha,alpha-trehalase
C:Keywords: glycosidase; hydrolase

Query Match 2.9%; Score 8; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLGIGL 23
|||||
DB 11 LLLLGIGL 18

RESULT 27
T00073
hypothetical protein KIA0527 - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
C:Accession: T00073
R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara,
DNA Res. 5, 31-39, 1998

A:Title: Prediction of the coding sequences of unidentified human genes. IX. The comp
A:Reference number: Z14086; MUID:98290545
A:Accession: T00073

A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-768 <NAG>
A:Cross-references: EMBL:AB011099; NID:g3043577; PIDN:BAA25453.1; PID:g3043578
A:Experimental source: brain; clone HG2246
C:Genetics:
A>Note: KIA0527

Query Match 2.9%; Score 8; DB 2; Length 768;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 AALLLIGL 21
|||||
DB 161 AALLLIGL 168

RESULT 28
T06130
hypothetical protein F23E12.170 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 30-Apr-1998 #sequence_revision 30-Apr-1999 #text_change 15-Sep-2000
C:Accession: T06130
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Hoheis
submitted to the Protein Sequence Database, April 1999
A:Reference number: Z15485
A:Accession: T06130
A:Molecule type: DNA
A:Residues: 1-1031 <BEV>
A:Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.170
A:Experimental source: cultivar Columbia; BAC clone F23E12
C:Genetics:
A:Gene: ATSP:F23E12.170
A:Map position: 4
A:Introns: 307/3; 359/2; 682/1; 898/3; 962/1
C:Superfamily: Arabidopsis thaliana hypothetical protein F23E12.170

Query Match 2.9%; Score 8; DB 2; Length 1031;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 PRTSOGPS 203
|||||
DB 143 PRTSOGPS 150

RESULT 29
T01742
hypothetical protein 3 - maize mitochondrion
C:Species: mitochondrion Zea mays (maize)
C>Date: 19-Feb-1999 #sequence_revision 19-Feb-1999 #text_change 29-Oct-1999
C:Accession: T01742
R:Smith, A.G.; Ping, D.R.
Curr. Genet. 12, 617-623, 1987
A:Title: Nucleotide sequence and molecular characterization of a maize mitochondrial
A:Reference number: Z14414; MUID:89003167
A:Accession: T01742
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-52 <SMI>

A:Cross-references: EMBL:M36398; NID:g342649; PIDN:AAA70277.1; PID:g897626
C:Genetics:
A:Genome: mitochondrion
C:Keywords: mitochondrion

Query Match 2.5%; Score 7; DB 2; Length 52;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 RRLGRGP 12
|||||||
Db 35 RRLGRGP 41

RESULT 30
T08512

trbO protein - Enterobacter aerogenes plasmid R751

C:Species: Enterobacter aerogenes

C>Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000

C:Accession: T08512

R:Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.

Plasmid 36, 95-111, 1996

A>Title: Conservation of the genetic switch between replication and transfer genes of In

A:Reference number: Z16434; MUID:97118926

A:Accession: T08512

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-88 <THO>

A:Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64456.1; PID:g1572561

C:Genetics:

A:Gene: trbO

A:Genome: plasmid R751

Query Match

Best Local Similarity 2.5%; Score 7; DB 2; Length 88;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLLGIG 22
|||||||
Db 36 LLLLGIG 42

Search completed: June 18, 2002, 14:29:51
Job time: 209 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:28:52 ; Search time 13.06 Seconds
(without alignments)
821.234 Million cell updates/sec

Title: US-09-852-845-2

Perfect score: 277

Sequence: 1 MCVGARRLRGPCPALILIG.....SFRPIQEQADAHSTLAKI 277

Scoring table: OLIGO

Searched: 105224 seqs, 38719550 residues

Word size : 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277	100.0	277	1	TNRA_HUMAN
2	12	4.3	271	1	TNRA_RAT
3	12	4.3	272	1	TNRA_MOUSE
4	9	3.2	625	1	TR11_MOUSE
5	8	2.9	78	1	PUPX_RHOCA
6	8	2.9	394	1	Y6B9_PSEAE
7	8	2.9	445	1	YUDE_ECOLI
8	8	2.9	575	1	CTDD_BACSU
9	8	2.9	578	1	TREA_RABIT
10	8	2.9	583	1	TREA_HUMAN
11	7	2.5	91	1	NULM_BRALA
12	7	2.5	96	1	GRO_MOUSE
13	7	2.5	101	1	ELAB_ECOLI
14	7	2.5	119	1	H1B_PLAUD
15	7	2.5	144	1	CYTF_MOUSE
16	7	2.5	164	1	PR12_HORVU
17	7	2.5	164	1	PR1_HORVU
18	7	2.5	173	1	GRAM_MOUSE
19	7	2.5	173	1	NU6M_MOUSE
20	7	2.5	173	1	NU6M_ONCRY
21	7	2.5	173	1	NU6M_SALSA
22	7	2.5	200	1	NO6A_PARDE
23	7	2.5	265	1	HA2Q_HUMAN
24	7	2.5	265	1	BXB1_HAEIN
25	7	2.5	265	1	BXB3_HAEIN
26	7	2.5	267	1	Y6B9_HAEIN
27	7	2.5	269	1	LEP4_SYNT3
28	7	2.5	283	1	LEP4_ERWCH
29	7	2.5	298	1	VBL1_CLVK
30	7	2.5	298	1	VBL1_CLVN
31	7	2.5	327	1	DHBI_HUMAN
32	7	2.5	342	1	ISIA_SYND2
33	7	2.5	354	1	CD68_HUMAN

34	7	2.5	371	1	YAOS_RHISN	P55604 rhizobium s
35	7	2.5	373	1	YU2_PICAN	P34735 pichia angu
36	7	2.5	377	1	Y4WD_RHISN	P55682 rhizobium s
37	7	2.5	389	1	Y596_MYCTU	Q10817 mycobacteri
38	7	2.5	415	1	CRF1_MOUSE	P35347 mus musculu
39	7	2.5	415	1	CRF1_RAT	P35353 rattus norv
40	7	2.5	415	1	CRF1_SHEEP	O62772 ovys aries
41	7	2.5	428	1	NSD1_PSEAE	O9HY11 pseudomonas
42	7	2.5	438	1	NMT2_PSEAE	O9YF2 pseudomonas
43	7	2.5	441	1	ODBA_RAT	P11960 rattus norv
44	7	2.5	442	1	ODBA_MOUSE	P50136 mus musculu
45	7	2.5	444	1	CRF1_HUMAN	P34998 homo sapien
46	7	2.5	468	1	YB07_HAEIN	O57007 haemophilus
47	7	2.5	469	1	NCOO_THERH	O56228 thermus aqu
48	7	2.5	498	1	NFSL_SCHPO	O74351 schizosacch
49	7	2.5	548	1	ERF_HUMAN	P50548 homo sapien
50	7	2.5	551	1	ERF_MOUSE	P70459 mus musculu

ALIGNMENTS

RESULT 1
TNRA_HUMAN
ID P43489; Q13663; STANDARD: PRT; 277 AA.
AC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE receptor) (ACT35 antigen) (TAX-transcriptionally activated
DE glycoprotein 1 receptor) (CD134 antigen).
GN TNFRSF4 OR TNXP1L.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=94170844; PubMed=7510240;
RX Latza U., Dueckop H., Schultze S., Ringeling J., Eitelbach F.,
RA Hummel M., Fonatsch C., Stein H.,
RT "The human OX40 homolog: CDNA structure, expression and chromosomal
RT assignment of the ACT35 antigen."
RL Eur. J. Immunol. 24:677-683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=95219871; PubMed=7704935;
RA Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.,
RT "Identification of OX40 ligand and preliminary characterization of
RT its activities on OX40 receptor."
RL Cite. Shock 44:30-34(1994).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- DATABASE: NAME=PROT; NOTE=CD guide CD134 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X75962; CAA53576.1; -
CC EMBL: S76792; AAB33944.1; ALT_INIT.
CC HSSP: P25942; ICDF.
CC MIM: 600315; -
CC InterPro: IPR001368; TNFR_c6.
CC Pfam: PF00020; TNFR_c6; 3.
DR

DR Prodom: PD000771; TNFR_c6; 1.
 DR SMART; SMO0208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00500; TNFR_NGFR_2; 2.
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
 Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 277
 FT DOMAIN 29 214
 FT TRANSMEM 215 235
 FT DOMAIN 236 277
 FT REPEAT 30 65
 FT REPEAT 66 107
 FT REPEAT 108 126
 FT REPEAT 127 167
 FT CAROHD 146 146
 FT CAROHD 160 160
 SQ SEQUENCE 277 AA; 29340 MW; 49F13525941550BF CRC64;

Query Match 100.0%; Score 277; DB 1; Length 277;
 Best Local Similarity 100.0%; Pred. No. 2,66-263; Mismatches 0; Indels 0; Gaps 0;
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCVGARLRGRCPCALLLLGLSTVGLHGYDTPPSNDRCHCPCNGMVSRSQ 60
 DB 1 MCVGARLRGRCPCALLLLGLSTVGLHGYDTPPSNDRCHCPCNGMVSRSQ 60
 QY 61 MIVCRGCGGFNDVYSSPKCKPCMCNLRSGERKOLCTAODYCRCRAGOPIDSK 120
 DB 61 MIVCRGCGGFNDVYSSPKCKPCMCNLRSGERKOLCTAODYCRCRAGOPIDSK 120
 QY 121 PCVDCAPCPGHFSPDNOACKPMTNCTLAGKHTLOPASNSSDALCEDDPATOPQETO 180
 DB 121 PCVDCAPCPGHFSPDNOACKPMTNCTLAGKHTLOPASNSSDALCEDDPATOPQETO 180
 QY 181 GPPARITVQPTLEAWPRTSGSPSTRVEYPPGGRVAAIIGLGLVGLLPLAILLALL 240
 DB 181 GPPARITVQPTLEAWPRTSGSPSTRVEYPPGGRVAAIIGLGLVGLLPLAILLALL 240
 QY 241 RRQRLPPDAHKPPGGSFRTPIQEQADAHSLAKI 277
 DB 241 RRQRLPPDAHKPPGGSFRTPIQEQADAHSLAKI 277

RESULT 2
 TNFR_RAT
 ID TNFR_RAT STANDARD: PRT: 271 AA.
 AC P15725:
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen) (MRC OX40).
 GN TNFRSF4 OR TXGP1L OR OX40.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=T-cell;
 RA MEDLINE=90214614; PubMed=2157591;
 RA Mallett S., Fossum S., Barclay A.N.;
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";
 RL EMBO J 9:1063-1068(1990)
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/ GP34 CYTOKINE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; X17037; CAA34897.1; -
 DR PIR; S08036; S08036.
 DR PIR; S12783; S12783.
 DR HSP; P19438; 1EXT.
 DR InterPro; IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR Prodom; PD000771; TNFR_c6; 1.
 DR SMART; SMO0208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; 3.
 DR PROSITE; PS00500; TNFR_NGFR_2; 2.
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
 Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 271
 FT DOMAIN 20 210
 FT TRANSMEM 211 235
 FT DOMAIN 236 271
 FT REPEAT 25 60
 FT REPEAT 61 102
 FT REPEAT 103 123
 FT REPEAT 124 164
 FT CAROHD 143 143
 SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 4.3%; Score 12; DB 1; Length 271;
 Best Local Similarity 100.0%; Pred. No. 0,00042; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPMTNCTL 149
 DB 135 NOACKPMTNCTL 146

RESULT 3
 TNFR_MOUSE
 ID TNFR_MOUSE STANDARD: PRT: 272 AA.
 AC P47741:
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen).
 GN TNFRSF4 OR TXGP1L OR OX40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C;
 RX MEDLINE=94044750; PubMed=8228223;
 RA Calderhead D.M., Buhlmann J.E., van den Eertwegh A.J.,
 RA Claassen E., Noelle R.J., Fell H.;
 RT "Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell interactions.";
 RL J. Immunol. 151:5261-5271(1993).
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/ GP34 CYTOKINE.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
 CC -----

```

RL Eur. J. Immunol. 25:926-930(1995).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: Z21674; CAA9772.1; -
DR EMBL: X85214; CAA59476.1; -
DR HSSP: P19438; EXT.
DR MGD: MGI:104512; Tnftrsf4.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR PRODOM: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR Receptor: T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 272
FT FT TUMOR NECROSIS FACTOR RECEPTOR
FT FT SUPERFAMILY MEMBER 4
FT FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 236
FT DOMAIN 237 272
FT REPEAT 26 61
FT REPEAT 62 103
FT REPEAT 104 124
FT REPEAT 125 165
FT CARBOHYD 144 144
FT CONFLICT 15 15
FT SEQUENCE 272 AA; 30153 MW; 06E7B84156FDD08E CRC64;
SQ
Query Match 4.3%; Score 12; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 NOACKPWTNCTL 149
Db 136 NOACKPWTNCTL 147
-----
RESULT 4
TR1L_MOUSE STANDARD; PRT; 625 AA.
ID TR1L_MOUSE
AC 035305;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11A precursor
DE (Receptor activator of NF-kB) (osteoclast differentiation factor
DE receptor) (ODFR).
GN TNFRSF11A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=fetal liver;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougal W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Gallibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
```

```

RL Nature 390:175-179(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=99097247; PubMed=9878548;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis."
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
CC -1- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS
CC OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-
CC MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
CC INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- TISSUE SPECIFICITY: UNBIOUITOUS EXPRESSION WITH HIGH LEVELS IN
CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: AF019046; AAB86810.1; -
DR HSSP: P25942; ICDF.
DR MGD: MGI:1314891; Tnftrsf11a.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR PRODOM: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR Receptor: Glycoprotein; Transmembrane; Repeat; Signal.
KW SIGNAL 1 30
FT FT TUMOR NECROSIS FACTOR RECEPTOR
FT FT SUPERFAMILY MEMBER 11A.
FT FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 234
FT DOMAIN 235 625
FT REPEAT 35 69
FT REPEAT 72 113
FT REPEAT 115 152
FT REPEAT 155 195
FT DISULFID 35 47
FT DISULFID 48 61
FT DISULFID 51 69
FT DISULFID 72 87
FT DISULFID 93 113
FT DISULFID 115 128
FT DISULFID 134 152
FT CARBOHYD 106 106
FT CARBOHYD 175 175
FT SEQUENCE 625 AA; 66621 MW; F8C1872E9511D8E CRC64;
SQ
Query Match 3.2%; Score 9; DB 1; Length 625;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 141 CKPWTNCTL 149
Db 170 CKPWTNCTL 178
-----
RESULT 5
PUFX_RHOCA STANDARD; PRT; 78 AA.
ID PUFX_RHOCA
AC P26240;
DT 01-MAY-1992 (Rel. 22, Created)
```

```

DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Intrinsic membrane protein pufX (Protein C2397).
GN PUFX.
OS Rhodobacter capsulatus (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Rhodobacter.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84259352; PubMed=6744416;
RA Youvan D.C., Bylina E.J., Alberti M., Begusch H., Hearst J.E.;
RT "Nucleotide and deduced polypeptide sequences of the photosynthetic
RT reaction-center, B870 antenna, and flanking polypeptides from R.
RT capsulata."
RL Cell 37:949-957(1984).
CC -1- FUNCTION: ASSOCIATED WITH THE REACTION CENTER - LIGHT-HARVESTING
CC COMPLEX I. MAY PLAY A CRITICAL ROLE IN FACILITATING THE
CC INTERACTION BETWEEN THIS COMPLEX AND OTHER COMPONENTS REQUIRED FOR
CC LIGHT-DRIVEN CYCLIC ELECTRON TRANSFER.
CC -1- SUBCELLULAR LOCATION: INTRACRYSTALLINE MEMBRANE.
CC -1- SIMILARITY: TO PUFX FROM R. SPHEROIDES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: Z11165; CAN7556.1; -
DR EMBL: K01183; -; NOT_ANNOTATED_CDS.
DR PIR: F28771; F28771.
DR Photosynthesis; Membrane.
SQ SEQUENCE 78 AA; 8569 MW; D85FF4097E5D65B0 CRC64;

Query Match
Best Local Similarity 2.9%; Score 8; DB 1; Length 78;
Matches 8; Conservative 100.0%; Pred. No. 1.2;
Mismatch 0; Indels 0; Gaps 0;

QY 219 LGGLVGLG 226
DB 39 LGGLVGLG 46

RESULT 6
Y6B9_PSEAE STANDARD; PRT; 394 AA.
AC P42514;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein PA4219.
GN PA4219.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PAO1;
RX MEDLINE=94117363; PubMed=8288523;
RA Ankenbauer R.G., Quan H.N.;
RT "Fpca, the Fe(II)-pyochelin receptor of Pseudomonas aeruginosa: a
RT phenolate siderophore receptor homologous to hydroxamate siderophore
RT receptors."
RL J. Bacteriol. 176:307-319(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;

```

```

RA Stoyer C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.J., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: U03161; AAC43215.1; -
DR EMBL: AE004838; AAG07607.1; -
DR Hypothetical protein; Transmembrane; Complete proteome.
KM TRANSMEM 22 42
FT TRANSMEM 60 80 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 231 251 POTENTIAL.
FT TRANSMEM 271 291 POTENTIAL.
FT TRANSMEM 303 323 POTENTIAL.
FT TRANSMEM 328 348 POTENTIAL.
FT TRANSMEM 355 375 POTENTIAL.
SQ SEQUENCE 394 AA; 42248 MW; 89A0D93871CC71BE CRC64;

Query Match
Best Local Similarity 2.9%; Score 8; DB 1; Length 394;
Matches 8; Conservative 100.0%; Pred. No. 4.8;
Mismatch 0; Indels 0; Gaps 0;

QY 14 AALLLGL 21
DB 280 AALLLGL 287

RESULT 7
YUDE_ECOLI STANDARD; PRT; 445 AA.
AC P39269; P39268;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical transport protein yude.
GN YUDE OR B4115 OR Z5717 OR ECSS097.
OS Escherichia coli.
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=9534362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes."
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2]
RP REVISIONS.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;

```

RT "The complete genome sequence of Escherichia coli K-12."
 RL Science 277:1453-1474(1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-0157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE-21074935; PubMed-11206551;
 RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobeck E.J., Davis N.W., Lam A., Dimalanta E.T., Potamoustis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";
 RL Nature 409:529-533(2001).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-0157:H7 / RIMD 0509952;
 RX MEDLINE-21156231; PubMed-11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakiwa C., Ogasawara N., Yasunaga T.,
 RA Kihara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 O157:H7 and genomic comparison with a laboratory strain K-12";
 RL DNA Res. 8:11-22(2001).
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
 (potential).
 CC -1 SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF
 PERMEASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: U14003; AAA97015.1; ALT_FRAME.
 DR EMBL: U14003; AAA97014.1; ALT_FRAME.
 DR EMBL: AE000484; AAC77076.1; -
 DR EMBL: AE005644; AAC59314.1; -
 DR EMBL: AP002368; BAB38520.1; -
 DR EcoGene; EG12462; yjde.
 DR InterPro: IPR002293; AA_rel_permease_1.
 DR InterPro: IPR002027; Amino_acid_permease.
 DR Pfam; PF00324; aa-permeases; 1.
 KW Hypothetical protein; Transpore; Transmembrane; Inner membrane;
 KW Complete proteome.
 FT TRANSMEM 10 30 POTENTIAL.
 FT TRANSMEM 39 59 POTENTIAL.
 FT TRANSMEM 99 119 POTENTIAL.
 FT TRANSMEM 123 143 POTENTIAL.
 FT TRANSMEM 153 173 POTENTIAL.
 FT TRANSMEM 197 217 POTENTIAL.
 FT TRANSMEM 226 246 POTENTIAL.
 FT TRANSMEM 276 296 POTENTIAL.
 FT TRANSMEM 322 342 POTENTIAL.
 FT TRANSMEM 356 376 POTENTIAL.
 FT TRANSMEM 386 406 POTENTIAL.
 FT TRANSMEM 409 429 POTENTIAL.
 SQ SEQUENCE 445 AA; 46842 MW; 359F70C489A20663 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 445;
 Best Local Similarity 100.0%; Pred. No. 5.3;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CAALLLG 20
 |||||
 DB 369 CAALLLG 376

RESULT 8
 ID CYDD_BACSU STANDARD; PRT: 575 AA.
 AC P94367;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Transport ATP-binding protein cydD.
 GN CYDD.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;
 OC Bacillus/Staphylococcus group; Bacillus.
 OX NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-168 / BGSCL1;
 RX MEDLINE-97124196; PubMed-8969509;
 RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,
 RA Miwa Y., Fujita Y.;
 RT "Sequencing of a 65 kb region of the Bacillus subtilis genome
 containing the *lic* and *cel* loci, and creation of a 177 kb contig
 covering the *gnt-sacXy* region";
 RL Microbiology 142:3113-3123(1996).
 CC -1 FUNCTION: SOMEHOW INVOLVED IN THE CYTOCHROME D BRANCH OF AEROBIC
 CC RESPIRATION. SEEMS TO BE A COMPONENT OF A TRANSPORT SYSTEM (BY
 CC SIMILARITY).
 CC -1 SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1 SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D83026; BAA11730.1; -
 DR EMBL: Z99123; CAB15899.1; -
 DR HSSP: P13569; INBD.
 DR Subtilist; BG11928; cydD.
 DR InterPro: IPR003593; AAA.
 DR InterPro: IPR001140; ABC_transporter_tmam.
 DR InterPro: IPR003439; ABC_transporter.
 DR InterPro: IPR001687; ATP_GTP_A.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport; Transmembrane; Complete proteome.
 FT TRANSMEM 17 37 POTENTIAL.
 FT TRANSMEM 53 73 POTENTIAL.
 FT TRANSMEM 135 155 POTENTIAL.
 FT TRANSMEM 161 181 POTENTIAL.
 FT TRANSMEM 246 266 POTENTIAL.
 FT TRANSMEM 275 295 POTENTIAL.
 FT NP_BIND 370 377 ATP (POTENTIAL).
 SQ SEQUENCE 575 AA; 64509 MW; FFI7B481DF22A0BF CRC64;

Query Match 2.9%; Score 8; DB 1; Length 575;
 Best Local Similarity 100.0%; Pred. No. 6.6;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 232 ATLALYL 239
 |||||
 DB 160 ATLALYL 167

RESULT 9
 TREA_RABIT STANDARD; PRT: 578 AA.
 ID TREA_RABIT
 AC P19813;

DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Trehalase precursor (EC 3.2.1.28) (Alpha, alpha-trehalase)
DE (Alpha, alpha-trehalose glucosyltransferase).
GN Treh OR TREA.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=NEW ZEALAND WHITE.
RX MEDLINE=90368681; PubMed=1697585;
RA Ruf J., Macker H., James P., Maffia M., Sella P., Geland G.,
RA von Kleebeckus A., Semenza G., Mantel N.;
RT "Rabbit small intestinal trehalase. Purification, cDNA cloning,
RT expression, and verification of glycosylphosphatidylinositol
RT anchoring.";
RL J. Biol. Chem. 265:15034-15039(1990).
CC -1- FUNCTION: INTESTINAL TREHALASE IS PROBABLY INVOLVED IN THE
CC HYDROLYSIS OF INGESTED TREHALOSE.
CC -1- CATALYTIC ACTIVITY: Alpha, alpha-trehalose + H(2)O = 2 D-glucose.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- TISSUE SPECIFICITY: SMALL INTESTINE, KIDNEY, AND LESSER IN LIVER.
CC -1- SIMILARITY: BELONGS TO FAMILY 37 OF GLYCOSYL HYDROLASES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: M55299; AAA63460.1; -
DR PIR: A35810; A35810.
DR InterPro: IPR001661; Trehalase.
DR Pfam: PF01204; Trehalase.1.
DR PRINTS: PR00744; GLHYDRASE37.
DR PROSITE: PS00927; TREHALASE.1; 1.
DR PROSITE: PS00928; TREHALASE.2; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Signal; GPI-anchor.
FT SIGNAL 1 19
FT CHAIN 20 558
FT PROPEP 559 578
FT LIPID 558 558
FT CARBOHYD 78 78
FT CARBOHYD 261 261
FT CARBOHYD 369 369
FT CARBOHYD 417 417
SQ SEQUENCE 578 AA: 65517 MW: 9014B1189818CEAC CRC64;
OR 20, OR 22 (POTENTIAL).
TREA_HUMAN
ID TREA_HUMAN STANDARD: PRT: 583 AA.
AC 043280:
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Trehalase precursor (EC 3.2.1.28) (Alpha, alpha-trehalase)
DE (Alpha, alpha-trehalose glucosyltransferase).
Query Match 2.9%; Score 8; DB 1; Length 578;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16 LLLLGGL 23
DB 11 LLLLGGL 18

GN Treh OR TREA.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98087419; PubMed=9427547;
RA Ishihara R., Taketani S., Sasai-Takedatsu M., Kino M., Tokunaga R.,
RA Kobayashi Y.,
RT "Molecular cloning, sequencing and expression of cDNA encoding human
RT trehalase.";
RL Gene 202:69-74(1997).
RN [2]
RP PARTIAL SEQUENCE.
RX MEDLINE=96369335; PubMed=8773341;
RA Sasai-Takedatsu M., Taketani S., Nagata N., Furukawa T., Tokunaga R.,
RA Kojima T., Kobayashi Y.;
RT "Human trehalase: characterization, localization, and its increase in
RT urine by renal proximal tubular damage.";
RL Nephron 73:179-185(1996).
CC -1- FUNCTION: INTESTINAL TREHALASE IS PROBABLY INVOLVED IN THE
CC HYDROLYSIS OF INGESTED TREHALOSE.
CC -1- CATALYTIC ACTIVITY: Alpha, alpha-trehalose + H(2)O = 2 D-glucose.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -1- SIMILARITY: BELONGS TO FAMILY 37 OF GLYCOSYL HYDROLASES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL: AB000824; BAA24381.1; -
DR MIM: 275360; -
DR InterPro: IPR001661; Trehalase.
DR Pfam: PF01204; Trehalase.1.
DR PRINTS: PR00744; GLHYDRASE37.
DR PROSITE: PS00927; TREHALASE.1; 1.
DR PROSITE: PS00928; TREHALASE.2; 1.
KM Hydrolyase; Glycosidase; Glycoprotein; Signal; GPI-anchor.
FT SIGNAL 1 19
FT CHAIN 20 559
FT PROPEP 560 583
FT LIPID 559 559
FT CARBOHYD 78 78
FT CARBOHYD 239 239
FT CARBOHYD 261 261
FT CARBOHYD 369 369
SQ SEQUENCE 583 AA: 66596 MW: 3EE4D31BD4D243A9 CRC64;
OR 20, OR 21 (POTENTIAL).
NUTM_BRA
ID NUTM_BRA STANDARD: PRT: 91 AA.
AC 079420; 047424;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).
Query Match 2.9%; Score 8; DB 1; Length 583;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 16 LLLLGGL 23
DB 11 LLLLGGL 18

```

GN ND4L OR NAD4L OR NAD4L.
OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus), and
OC Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7740, 7739;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Branchiostoma lanceolatum;
RX MEDLINE=96292550; PubMed=9628930;
RA Spruyt N., Delabre C., Gachein G., Laudet V.;
RT "Complete sequence of the amphioxus (Branchiostoma lanceolatum)
RT mitochondrial genome: relations to vertebrates.";
RL Nucleic Acids Res. 26:3279-3285(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Branchiostoma floridae;
RX MEDLINE=99261652; PubMed=10331267;
RA Boore J.L., Daehler L.L., Brown W.M.;
RT "Complete sequence, gene arrangement, and genetic code of
RT mitochondrial DNA of the cephalochordate Branchiostoma floridae
RT (Amphioxus).";
RL Mol. Biol. Evol. 16:410-418(1999).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: Y16474; CAA76255.1; -
DR EMBL: AF098298; AAB87993.2; -
DR InterPro: IPR003214; Mlt_NADH_oxidoreductase_4L.
DR InterPro: IPR001133; Oxidored_q2.
DR Pfam: PF00420; oxidored_q2; 1.
DR ProDom: PD000359; Mlt_NADH_oxidoreductase_4L; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 91 AA; 9751 MW; 7E7D093F02468BD3 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 LGLGLS 24
|111111|
Db 12 LGLGLS 18

RESULT 12
GRO_MOUSE STANDARD; PRT; 96 AA.
ID GRO_MOUSE
AC P12850;
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth regulated protein precursor (Platelet-derived growth factor-
DE inducible protein KC) (Secretory protein N51).
GN SCVB1 OR GRO1 OR GRO OR MSCA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=69139485; PubMed=2917992;
RX Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;
RA "The platelet-derived growth factor-inducible KC gene encodes a
RT secretory protein related to platelet alpha-granule proteins.";

```

```

RL J. Biol. Chem. 264:4133-4137(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89078502; PubMed=2909392;
RA Ryseck R.P., Macdonald-Bravo H., Mallet M.-G., Bravo R.;
RT "Cloning and sequence of a secretory protein induced by growth
RT factors in mouse fibroblasts.";
RL Exp. Cell Res. 180:266-275(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Bozic C.M., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M.,
RA Conklyn M.J., Breslow R., Howell H.J., Gerard N.P., Gerard C.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96016008; PubMed=7561058;
RA Ohmori Y., Fukumoto S., Hamilton T.A.;
RT "Two structurally distinct kappa B sequence motifs cooperatively
RT control LPS-induced KC gene transcription in mouse macrophages.";
RL J. Immunol. 155:3593-3600(1995).
CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO
CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).
CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY
CC LIPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@lsb-sib.ch).
CC -----
DR EMBL: J04596; AAA40131.1; -
DR EMBL: U20634; AAB03376.1; -
DR EMBL: U20527; AAB03376.1; JOINED.
DR EMBL: S79767; -; NOT_ANNOTATED_CDS.
DR PIR: A32954; A32954.
DR PIR: A32954; A32954.
DR HSSP: P19875; 10NK.
DR MGD: MGI:108068; Gro1.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; Small_cytokine_CXC.
DR Pfam: PF00048; IL8; 1.
DR PRINTS; PR00437; SMALLCYTRCXC.
DR SMART; SM00199; SCY; 1.
DR PROSITE; PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 24
FT CHAIN 1 26 PROBABLE.
FT DISULFID 33 59 GROWTH REGULATED PROTEIN.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 96 AA; 10254 MW; 4A52B5E5C38BA5C2 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CAALLL 19
|111111|
Db 10 CAALLL 16

RESULT 13
ELAB_ECOLI STANDARD; PRT; 101 AA.
ID ELAB_ECOLI
AC P52084; Q47010;
DT 01-OCT-1996 (Rel. 34, Created)

```

DT 01-NOV-1997 (Rel. 35, last sequence update)
 DT 16-OCT-2001 (Rel. 40, last annotation update)
 DE Elab protein.
 GN ELAB OR B2266 OR Z3526 OR ECS3154.
 OS Escherichia coli. and
 OS Escherichia coli O157:H7.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Escherichia.
 OX NCBI_TaxID=562, 83334;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RA Hulsmann G.W.;
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474 (1997).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12;
 RX MEDLINE=97349980; PubMed=9205837;
 RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,
 RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
 RA Oshima T., Oyama S., Saito N., Stampel G., Satoh Y., Sivasubraman S.,
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
 RA Yamagata S., Horikuchi T.;
 RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
 RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and
 RT analysis of its sequence features.";
 RL DNA Res. 4:91-113 (1997).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-K12 / MC4100;
 RX MEDLINE=96140724; PubMed=8549818;
 RA Mueller R., Dahm C., Schulte G., Leitner E.;
 RT "An isochorismate hydroxymutase isogene in Escherichia coli.";
 RL PEBB Lett. 378:131-134 (1996).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-O157:H7 / EDL933 / ATCC 700927;
 RX MEDLINE=21074935; PubMed=11206551;
 RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
 RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
 RA Welch R.A., Blattner F.R.;
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
 RL Nature 409:529-533 (2001).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN-O157:H7 / RIMD 0509952;
 RX MEDLINE=21156231; PubMed=11258796;
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
 RA Han C.-G., Ohnishi E., Nakayama K., Murata T., Tanaka M., Tobe T.,
 RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli
 RT O157:H7 and genomic comparison with a laboratory strain K-12.";
 RL DNA Res. 8:111-221 (2001).
 RN [7]
 RP IDENTIFICATION.
 RA Rud K.E.;
 RL Unpublished observations (MAR-1996).
 CC -1- SIMILARITY: STRONG, TO E.COLI YGAM AND YGJD.

CC -1- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 CC FRAMESHIFT IN POSITION 73.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U58768; AAB02730.1; -;
 DR EMBL: AE000316; AAC75326.1; -;
 DR EMBL: D90858; CAB22026.1; -;
 DR EMBL: D90857; CAB22016.1; -;
 DR EMBL: Z50849; -; NOT_ANNOTATED_CDS.
 DR EMBL: AE005459; AAG57399.1; -;
 DR EMBL: AP002561; BAB36577.1; -;
 DR Ecogene: EG13185; elab.
 KW Complete proteome.
 SQ SEQUENCE 101 AA; 11306 MW; B934EB15C373CF6F CRC64;

QY Query Match 2.5%; Score 7; DB 1; Length 101;
 Db Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 222 GLVLGL 228
 Db 91 GLVLGL 97

RESULT 14
 H1B_PLADU STANDARD; PRT: 119 AA.
 ID H1B_PLADU
 AC P06895;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Histone H1B, sperm.
 OS Platynereis dumerilii (Dumeril's clam worm).
 CC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;
 CC Phyllococida; Nereididae; Platynereis.
 OX NCBI_TaxID=6359;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85257663; PubMed=4018088;
 RA Kmiecik D., Sellas D., Belaische D., Sautiere P.;
 RT "Primary structure of the two variants of a sperm-specific histone H1
 RT from the annelid Platynereis dumerilii.";
 RL Eur. J. Biochem. 150:359-370 (1985).
 CC -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
 CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
 DR PIR: B24560; HSDIB.
 DR HSP: P02259; IHST.
 DR InterPro: IPR001386; Linker_histone.
 DR InterPro: IPR003216; Linkerhist_N.
 DR Pfam: PF00538; Linker_histone_1.
 DR ProDom: PD000373; Linkerhist_N_1.
 DR SMART: SM00526; H15; 1.
 KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
 KW Sperm.
 FT DOMAIN 7 77 GLOBULAR.
 SQ SEQUENCE 119 AA; 13099 MW; CA18E93EE5963858 CRC64;

QY Query Match 2.5%; Score 7; DB 1; Length 119;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 215 VAAIIGL 221

Db 17 VAAITGL 23

RESULT 15

CYTF_MOUSE

STANDARD; PRT; 144 AA.

AC 089098;

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Cystatin F precursor (leukocystatin) (Cystatin 7) (Cystatin-like

metastasis-associated protein) (CMAP).

OS CST7.

GN Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=98298157; PubMed=9632704;

RA Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,

RA Xu Y., Weiss M., Ikeda M., Liggett D., Helms A., Caux C., Lebecque S.,

RA Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.;

RT "Leukocystatin, a new class II cystatin expressed selectively by

hematopoietic cells."

RL J. Biol. Chem. 273:16400-16408(1998).

CC -1- FUNCTION: INHIBITS PAPAIN AND CATHEPSIN L BUT WITH AFFINITIES

LOWER THAN OTHER CYSTATINS. MAY PLAY A ROLE IN IMMUNE REGULATION

THROUGH INHIBITION OF A UNIQUE TARGET IN THE HEMATOPOIETIC SYSTEM.

CC -1- SUBCELLULAR LOCATION: Secreted (Probable).

CC -1- SIMILARITY: BELONGS TO THE CYSTATIN FAMILY.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; AF031826; AAC40140.1; -

DR EMBL; AF031825; AAC40139.1; -

DR HSSP; P01038; 1A90.

DR MGD; MGI:1298217; Cst7.

DR InterPro: IPR000010; Cystatin.

DR InterPro: IPR003243; Cystatin_C_M.

DR Pfam; PF00031; cystatin; 1.

DR SMART; SM00043; CY; 1.

DR PROSITE; PS00287; CYSTATIN; FALSE.NEG.

KW Thiol protease inhibitor; Glycoprotein; Signal.

FT SIGNAL

FT CHAIN

FT ACT_SITE

FT SITE

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

AC P35792;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Pathogenesis-related protein PR1-2 precursor.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Hordeum.

OX NCBI_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=CV. PSARKON RESISTANT; TISSUE=Leaf;

RA MEDLINE=95036024; PubMed=7524728;

RA Mouradov A., Mouradova E., Scott K.J.;

RT "Gene family encoding basic pathogenesis-related 1 proteins in

barley."

RL Plant Mol. Biol. 26:503-507(1994).

CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS

CC AGAINST PATHOGENS.

CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Z26320; CAA81229.1; -

DR PIR; S37188; S37188.

DR HSSP; P04284; ICFE.

DR InterPro: IPR001283; SCP.

DR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00837; V5PPXLIKE.

DR SMART; SM00198; SCP; 1.

DR PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.

DR PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.

KW Pathogenesis-related protein; Signal; Multigene family.

FT SIGNAL

FT CHAIN

FT MOD_RES

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

AC P35792;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Pathogenesis-related protein PR1-2 precursor.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Hordeum.

OX NCBI_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=CV. PSARKON RESISTANT; TISSUE=Leaf;

RA MEDLINE=95036024; PubMed=7524728;

RA Mouradov A., Mouradova E., Scott K.J.;

RT "Gene family encoding basic pathogenesis-related 1 proteins in

barley."

RL Plant Mol. Biol. 26:503-507(1994).

CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS

CC AGAINST PATHOGENS.

CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Z26320; CAA81229.1; -

DR PIR; S37188; S37188.

DR HSSP; P04284; ICFE.

DR InterPro: IPR001283; SCP.

DR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00837; V5PPXLIKE.

DR SMART; SM00198; SCP; 1.

DR PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.

DR PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.

KW Pathogenesis-related protein; Signal; Multigene family.

FT SIGNAL

FT CHAIN

FT MOD_RES

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

AC P35792;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Pathogenesis-related protein PR1-2 precursor.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Hordeum.

OX NCBI_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=CV. PSARKON RESISTANT; TISSUE=Leaf;

RA MEDLINE=95036024; PubMed=7524728;

RA Mouradov A., Mouradova E., Scott K.J.;

RT "Gene family encoding basic pathogenesis-related 1 proteins in

barley."

RL Plant Mol. Biol. 26:503-507(1994).

CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS

CC AGAINST PATHOGENS.

CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

CC -----

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; Z26320; CAA81229.1; -

DR PIR; S37188; S37188.

DR HSSP; P04284; ICFE.

DR InterPro: IPR001283; SCP.

DR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00837; V5PPXLIKE.

DR SMART; SM00198; SCP; 1.

DR PROSITE; PS01009; SCP_AG5_PRL_SC7_1; 1.

DR PROSITE; PS01010; SCP_AG5_PRL_SC7_2; 1.

KW Pathogenesis-related protein; Signal; Multigene family.

FT SIGNAL

FT CHAIN

FT MOD_RES

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

FT DISULFID

```

RM [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-94033324; PubMed-8219079;
RA Muradov A., Petrisovits L., Davidson A., Scott K.J.;
RT "A cDNA clone for a pathogenesis-related protein 1 from barley.";
RL Plant Mol. Biol. 23:439-442(1993).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/PPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z21494; CAA79703.1; -
DR PIR; S32002; S32002.
DR PIR; S39474; S39474.
DR HSSP; P04284; ICPE.
DR InterPro: IPR001283; SCP.
DR Pfam: PF00188; SCP: 1.
DR PRINTS: PR00837; V5TPXLIKE.
DR SMART; SM00198; SCP: 1.
DR PROSITE; PS01009; SCP_AG5_PRI_SCP_1; 1.
DR PROSITE; PS01010; SCP_AG5_PRI_SCP_2; 1.
DR Pathogenesis-related protein; Signal; Multigene family.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 1 25 PYROLIDONE CARBOXYLIC ACID
FT MOD_RES 25 25
FT FT 68 140
FT DISULFD 113 119 BY SIMILARITY.
FT FT 135 150 BY SIMILARITY.
FT DISULFD 135 150 BY SIMILARITY.
SQ SEQUENCE 164 AA; 17683 MW; 80972FF654F7395 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 231 LALLAL 237
DB 6 LALLAL 12

RESULT 18
GRAM_MOUSE STANDARD: PRT: 173 AA.
ID GRAM_MOUSE STANDARD: PRT: 173 AA.
AC P51437;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cathelin-related antimicrobial peptide precursor (Cramp) (Cathelin-
DE like protein) (CLP).
GN CNLP OR CRAMP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-C57BL/6; TISSUE=Bone marrow;
RA MEDLINE-97294716; PubMed-9148921;
RA Gallo R.L., Kim K.J., Bernfield M., Kozak C.A., Zanetti M.,
RA Merluzzi L., Gennaro R.;
RT "Identification of CRAMP, a cathelin-related antimicrobial peptide
RT expressed in the embryonic and adult mouse.";
RL J. Biol. Chem. 272:13088-13093(1997).
RN [2]

```

```

RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Bone marrow;
RX MEDLINE-96326596; PubMed-8706928;
RA Popueva A.E., Zinovjeva M.V., Vlaser Y.W.M., Fibbe W.E.,
RA Belyavsky A.V.;
RT "A novel murine cathelin-like protein expressed in bone marrow.";
RL FEBS Lett. 391:5-8(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-129/SVJ;
RA Hutterer K.M., Pirano J., Gallo R.L.;
RL Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: ACTS AS A POTENT ANTIMICROBIAL PEPTIDE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN TESTIS, SPLEEN, STOMACH, AND
CC INTERSTINE. VERY LOW EXPRESSION FOUND IN HEART, LUNG AND SKELETAL
CC MUSCLE. NO EXPRESSION IN BRAIN, KIDNEY OR LIVER.
CC -1- SIMILARITY: BELONGS TO THE CATHELICIDINS FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U43409; AAA85898.1; -
DR EMBL; X94353; CAA64078.1; -
DR EMBL; AF035680; AAB88303.1; -
DR HSSP; P25230; ILYP.
DR MGD; MGI:108443; CNLP.
DR InterPro: IPR001694; Cathelicidin.
DR Pfam; PF00666; Cathelicidins; 1.
DR ProDom; PD001838; Cathelicidin; 1.
DR PROSITE; PS00946; CATHELICIDINS_1; 1.
DR PROSITE; PS00947; CATHELICIDINS_2; 1.
DR Antiheliotic; Signal.
FT SIGNAL 1 27
FT PROPEP 28 139 POTENTIAL.
FT CHAIN 140 173 CATHELIN-RELATED ANTIMICROBIAL PEPTIDE.
FT MOD_RES 28 28 PYROLIDONE CARBOXYLIC ACID (BY
FT SIMILARITY).
FT FT 83 94 BY SIMILARITY.
FT DISULFD 105 122 BY SIMILARITY.
FT CONFLICT 24 24 L->M (IN REF. 2).
FT CONFLICT 173 173 MISSING (IN REF. 1).
SQ SEQUENCE 173 AA; 19581 MW; 143F0E784762E77E CRC64;

Query Match 2.5%; Score 7; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGLG 22
DB 19 LLLGLG 25

RESULT 19
NU6M_ONCMY STANDARD: PRT: 173 AA.
ID NU6M_ONCMY STANDARD: PRT: 173 AA.
AC P48177;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3).
GN MTND6 OR ND6.
OS Oncochrynechus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;

```

[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Liver;
RC MEDLINE=96139027; PubMed=8587139;
RA Zardoya R., Garrido-Perterra A., Bautista J.M.;
RT "The complete nucleotide sequence of the mitochondrial DNA genome of
RL J. Mol. Evol. 41:942-951(1995).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; L29771; AAB03358.1; -;
DR InterPro; IPR001457; Oxidored_q3.
DR Pfam; PF00499; oxidored_q3; 1.
KM Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 173 AA; 18144 MW; A02134BC15D0C3F CRC64;

Query Match 2.5%; Score 7; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 221 LGVLGL 227
Db 10 LGVLGL 16
|||||
ID NO6M_SALSA STANDARD; PRT; 173 AA.
NM06M_SALSA
AC Q92ZM2;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 6 (Ec 1.6.5.3).
GN NMND6 OR ND6 OR NADH6 OR NADH-6.
OS Salmo salar (Atlantic salmon).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX NCBI_TaxID=8030;
RN
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=20018174; PubMed=10548724;
RA Hurst C.D., Bartlett S.E., Davidson W.S., Bruce I.J.;
RT "The complete mitochondrial DNA sequence of the Atlantic salmon, Salmo
RL salar.";
RL Gene 239:237-242(1999).
RP
RP SEQUENCE FROM N.A.
RA Arnason U., Johnson E., Rasmussen A.S.;
RT "The complete mitochondrial genome sequence of a teleost, Salmo salar,
RL and comparisons with other salmoniformes.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC

DR EMBL; U12143; AAD04744.1; -;
DR EMBL; AF133701; AAF61389.1; -;
DR InterPro; IPR001457; Oxidored_q3.
DR Pfam; PF00499; oxidored_q3; 1.
KM Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 173 AA; 18388 MW; 55322B94E972CE17 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 221 LGVLGL 227
Db 10 LGVLGL 16
|||||
ID NOOA_PARDE STANDARD; PRT; 200 AA.
NM00A_PARDE
AC P29922;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 10 (Ec 1.6.5.3) (NADH
DE dehydrogenase 1, chain 10) (NDH-1, chain 10).
GN NQO10.
OS Paracoccus denitrificans.
OC Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC Paracoccus.
OX NCBI_TaxID=266;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13543;
RX MEDLINE=93136200; PubMed=8422400;
RA Xu X., Matsuno-Yagi A., Yagi T.;
RT "DNA sequencing of the seven remaining structural genes of the gene
RT cluster encoding the energy-transducing NADH-quinone oxidoreductase
RL of Paracoccus denitrificans.";
RL Biochemistry 32:968-981(1993).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC -1- SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNITS NQO7-14
CC CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: TO POLYPEPTIDE 6 OF THE NADH-UBIQUINOL OXIDOREDUCTASE
CC OF CHLOROPLASTS OR MITOCHONDRIA.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; L02354; AAA25596.1; -;
DR PIR; F45456; F45456.
DR InterPro; IPR001457; Oxidored_q3.
DR Pfam; PF00499; oxidored_q3; 1.
KM Oxidoreductase; NAD; Ubiquinone; Transmembrane.
RW TRANSMEM 22
FT TRANSMEM 26
FT TRANSMEM 46
FT TRANSMEM 51
FT TRANSMEM 71
FT TRANSMEM 90
FT TRANSMEM 110
FT TRANSMEM 144
FT TRANSMEM 164
FT TRANSMEM POTENTIAL.
SQ SEQUENCE 200 AA; 21819 MW; 903B421C3F4ACAE CRC64;

Query Match 2.5%; Score 7; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 219 LGVLGL 225

```

DB      133 LGGLVGL 139

RESULT  22
HA2Q_HUMAN STANDARD: PRT: 260 AA.
ID      HA2Q_HUMAN
AC      P20036; P01905;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      HLA class II histocompatibility antigen, DP alpha chain precursor
DE      (HLA-DPA1 alpha chain) (MHC class II DPA1-alpha) (DP(M4)).
GN      HLA-DPA1 OR HLA-SB.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=86041930; PubMed=2997750;
RA      Lawrence S.K., Das H.K., Pan J., Weissman S.M.;
RT      "The genomic organisation and nucleotide sequence of the HLA-SB(DP)
RT      alpha gene.";
RL      Nucleic Acids Res. 13:7515-7528(1985).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=87250502; PubMed=3036829;
RA      Gustafsson K., Widmark E., Jonsson A.-K., Servenius B., Sachs D.H.,
RA      Larhammar D., Raak L., Peterson P.A.;
RT      "Class II genes of the human major histocompatibility complex.
RT      Evolution of the DP region as deduced from nucleotide sequences of
RT      the four genes.";
RL      J. Biol. Chem. 262:8778-8786(1987).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=89053719; PubMed=2461352;
RA      Young J.A., Lindsey J., Bodmer J.G., Trowsdale J.;
RT      "Epitope recognition by a DP alpha chain-specific monoclonal antibody
RT      (DP11.1) is influenced by the interaction between the DP alpha chain
RT      and its polymorphic DP beta chain partner.";
RL      Hum. Immunol. 23:37-44(1988).
RN      [4]
RP      SEQUENCE OF 28-260 FROM N.A.
RA      MEDLINE=84168117; PubMed=6584734;
RA      Aulicay C., Lillie J.W., Arnott D., Grossberger D., Kappes D.,
RA      Strominger J.L.;
RT      "Isotypic and allotypic variation of human class II
RT      histocompatibility antigen alpha-chain genes.";
RL      Nature 308:327-333(1984).
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: X03100; CAA26887.1; -
DR      EMBL: M27487; AAA63220.1; -
DR      EMBL: X00457; CAA25143.1; -
DR      PIR: A02209; HLHUSB.
DR      PIR: A29313; A29313.
DR      HSSP: F01903; 2SEB.
DR      MIM: 142880; -
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003587; Ig_c1.
DR      InterPro: IPR001003; MHC_II_alpha.
DR      Pfam: PF00047; 1g_1.
DR      Pfam: PF00993; MHC_II_alpha; 1.
DR      SMART: SM00407; IGc1.1.
DR      PROSITE: PS00290; IG_MHC.1.

```

```

KM      MHC II: Transmembrane; Glycoprotein; Signal.
FT      SIGNAL 1 28
FT      CHAIN 29 260
FT      DOMAIN 29 115
FT      DOMAIN 116 209
FT      DOMAIN 210 222
FT      TRANSMEM 223 245
FT      DOMAIN 246 260
FT      DISULFID 138 194
FT      CAROHYD 109 109
FT      CAROHYD 149 149
FT      CONFLICT 237 237
SQ      SEQUENCE 260 AA; 29380 MM; 826174E963A8CB42 CRC64;

Query Match      2.5%; Score 7; DB 1; Length 260;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      221 LGGLVGL 227
      . | | | | |
DB      228 LGGLVGL 234

RESULT  23
BXBL_HAEIN STANDARD: PRT: 265 AA.
ID      BXBL_HAEIN
AC      P19390;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Capsule polysaccharide export inner-membrane protein bexb.
GN      BEXB.
OS      Haemophilus influenzae.
OC      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC      Haemophilus.
OX      NCBI_TaxID=727;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN=RM 153 / SEROTYPE B;
RA      MEDLINE=90170850; PubMed=2137816;
RA      Kroll J.S., Moxon E.R.;
RT      "Capsulation in distinctly related strains of Haemophilus influenzae
RT      type b: genetic drift and gene transfer at the capsulation locus.";
RL      J. Bacteriol. 172:1374-1379(1990).
CC      -1- FUNCTION: MAY FORM AN ATP-DRIVEN CAPSULE POLYSACCHARIDE EXPORT
CC      APPARATUS, IN ASSOCIATION WITH THE BEXA, BEXC AND BEXD PROTEINS.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC      (potential).
CC      -1- SIMILARITY: BELONGS TO THE ABC-2 SUBFAMILY OF INTEGRAL MEMBRANE
CC      PROTEINS.
CC      -1- SIMILARITY: 95% IDENTITY TO RM926 BEXB.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: M33787; AAA24945.1; -
DR      InterPro: IPR000412; ABC2_transport.
DR      Pfam: PF01061; ABC2_membrane; 1.
DR      PRINTS: PR00164; ABC2TRANSPO.
DR      PROSITE: PS00890; ABC2_MEMBRANE; 1.
KW      Polysaccharide transport; Transmembrane; Inner membrane.
FT      TRANSMEM 37 57
FT      TRANSMEM 64 84
FT      TRANSMEM 118 138
FT      TRANSMEM 151 171
FT      TRANSMEM 178 198

```

FT TRANSMEM 235 255 POTENTIAL.
SQ SEQUENCE 265 AA; 30181 MW; 0A436FF824CD25C1 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 265;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 ALLLIGL 21
|||||||
Db 246 ALLLIGL 252

RESULT 24
BXB3_HAEIN STANDARD; PRT; 265 AA.
ID BXB3_HAEIN
AC P22235;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Capsule polysaccharide export inner-membrane protein bexB.
GN BXB3.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_Taxid=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EAGAN / SEROTYPE B;
RX MEDLINE=91186821; PubMed=2082145;
RA Kroll J.S., Loynds B., Brophy L.N., Moxon E.R.;
RT "The bex locus in encapsulated Haemophilus influenzae: a chromosomal
RT region involved in capsule polysaccharide export.";
RL Mol. Microbiol. 4:1853-1862(1990).

CC -1- FUNCTION: MAY FORM AN ATP-DRIVEN CAPSULE POLYSACCHARIDE EXPORT
CC APPARATUS, IN ASSOCIATION WITH THE BEXA, BEXC AND BEXD PROTEINS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Potential).
CC -1- SIMILARITY: BELONGS TO THE ABC-2 SUBFAMILY OF INTEGRAL MEMBRANE
CC PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; X54987; CAA38733.1; -;
DR PIR; S12234; BWHIXB.
DR InterPro: IPR000412; ABC2_transport.
DR Pfam; PF01061; ABC2_membrane; 1.
DR PRINTS; PR00164; ABC2_TRANSPORT.
DR PROSITE; PS00890; ABC2_MEMBRANE; 1.
KW Polysaccharide transport; Transport; Transmembrane; Inner membrane.
FT TRANSMEM 37 57 POTENTIAL.
FT TRANSMEM 64 84 POTENTIAL.
FT TRANSMEM 118 138 POTENTIAL.
FT TRANSMEM 151 171 POTENTIAL.
FT TRANSMEM 178 198 POTENTIAL.
FT TRANSMEM 235 255 POTENTIAL.
SQ SEQUENCE 265 AA; 30195 MW; E3A4F181C4B3203E CRC64;

Query Match 2.5%; Score 7; DB 1; Length 265;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 ALLLIGL 21
|||||||
Db 246 ALLLIGL 252

RESULT 25

ID YG95_HAEIN STANDARD; PRT; 267 AA.
AC Q48215; Q05081;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Putative glycosyl transferase H11695 (EC 2.-.-.-).
GN H11695.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_Taxid=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A2;
RA McLaughlin R., Abu Kwaik Y., Young R., Spicola S., Apicella M.;
RT "Characterization and sequence of the lsg locus from Haemophilus
RT influenzae.";
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RC STRAIN=RD / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton B.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Sauder D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geophagen N.S.M.,
RA Gresham C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.,
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
DR EMBL; M94855; AAA24983.1; -;
DR EMBL; U32842; AAC23341.1; -;
DR TIGR; H11695; -;
DR InterPro: IPR001173; Glycos_transf_2.
DR Pfam; PF00535; Glycos_transf_2; 1.
KW Hypothetical protein; transferase; Glycosyltransferase;
KW Complete proteome.
FT CONFLICT 26 V -> G (IN REF. 1).
FT CONFLICT 46 D -> E (IN REF. 1).
FT CONFLICT 49 F -> S (IN REF. 1).
SQ SEQUENCE 267 AA; 30770 MW; A2F1A0532737D8C3 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 267;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 GNGWYSR 55
|||||||
Db 205 GNGWYSR 211

RESULT 26
LEP4_SYNY3 STANDARD; PRT; 269 AA.
ID LEP4_SYNY3
AC P72640;

```

DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type 4 preproliferin-like proteins leader peptide processing enzyme
DE [includes: leader peptidase (EC 3.4.99.-) (Preproliferin peptidase); N-
DE methyltransferase (EC 2.1.1.-)].
GN HOPD OR SLR1120.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K., Okumura S.,
RA Shimpou S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: CLEAVES TYPE-4 FIBRILLAR LEADER SEQUENCE AND METHYLATES
CC THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A24; ALSO KNOWN AS TYPE
CC III LEADER PEPTIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: D90899; BAA1642.1;
DR MEROPS: A24.004;
DR InterPro: IPR000045; Peptidase_C20.
DR Pfam: PF01478; Peptidase_C20; 1.
DR PRINTS: PR00864; PREPLMPRTASE.
KW Multifunctional enzyme; Hydrolase; Protease; Transferase;
KW Methyltransferase; Transmembrane; Complete proteome.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 100 120 POTENTIAL.
FT TRANSMEM 127 147 POTENTIAL.
FT TRANSMEM 154 174 POTENTIAL.
FT TRANSMEM 197 217 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
FT TRANSMEM 269 29767 MW; 4056E0AA9654B1C CRC64;
SQ SEQUENCE

Query Match 2.5%; Score 7; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 GLVLGL 228
DB 135 GLVLGL 141

RESULT 27
LEP4_ERWCH STANDARD; PRT; 283 AA.
ID LEP4_ERWCH
AC P31711;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type 4 preproliferin-like proteins leader peptide processing enzyme (Pectic
DE enzymes secretion protein outo) [includes: Leader peptidase
DE (EC 3.4.99.-) (Preproliferin peptidase); N-methyltransferase (EC 2.1.1.-)].
GN OUPD.
OS Erwinia chrysanthemi.

```

```

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=5556;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=EC16;
RX MEDLINE=93054355; PubMed=1429461;
RA Lindeberg M., Collmer A.;
RT "Analysis of eight out genes in a cluster required for pectic enzyme
RT secretion by Erwinia chrysanthemi: sequence comparison with secretion
RT genes from other Gram-negative bacteria.";
RL J. Bacteriol. 174:7385-7397(1992).
CC -1- FUNCTION: CLEAVES TYPE-4 FIBRILLAR LEADER SEQUENCE AND METHYLATES
CC THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A24; ALSO KNOWN AS TYPE
CC III LEADER PEPTIDASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sdb.ch/announce/
CC or send an email to license@sdb-sdb.ch).
CC -----
DR EMBL: L02214; AAA24841.1;
DR PIR: C47755; C47755.
DR MEROPS: A24.001;
DR InterPro: IPR000045; Peptidase_C20.
DR Pfam: PF01478; Peptidase_C20; 1.
DR PRINTS: PR00864; PREPLMPRTASE.
KW Multifunctional enzyme; Hydrolase; Protease; Transferase;
KW Methyltransferase; Transmembrane; Inner membrane.
FT TRANSMEM 13 33 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 216 236 POTENTIAL.
FT TRANSMEM 259 279 POTENTIAL.
FT TRANSMEM 283 31355 MW; 90B9CE722C4AA7E CRC64;
SQ SEQUENCE

Query Match 2.5%; Score 7; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ALLLGL 21
DB 17 ALLLGL 23

RESULT 28
Y635_METJA STANDARD; PRT; 283 AA.
ID Y635_METJA
AC Q58052;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0635.
GN MJ0635.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RX Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RX Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

```

RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodok A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.,
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RL Science 273:1058-1073(1996).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U67511; AAB98633.1; -
 DR TIGR; MJ0635; -
 KM Hypothetical protein; Complete proteome.
 SO SEQUENCE 283 AA; 32502 MW; 1CE52FC8457C5E20 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 283;
 Best Local Similarity 100.0%; Pred. No. 34;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 231 LAI1AL 237
 |||||
 Db 10 LAI1AL 16

RESULT 29
 VB1_CLVK STANDARD; PRT; 298 AA.
 AC P14981;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE B1 protein (33.7 kDa protein).
 GN BCL1.
 OS Cassava latent virus (strain West Kenya 844).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10818;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stanley J., Gay M.R.;
 RT "Nucleotide sequence of cassava latent virus DNA.";
 RL Nature 301:260-262(1983).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES B1 PROTEIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; J02058; -; NOT_ANNOTATED_CDS.
 DR InterPro; IPR000211; Gemini_B1.
 DR Pfam; PF00845; Gemini_B1; 1.
 SO SEQUENCE 298 AA; 33773 MW; D1E37C3F3B4CFPA5 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 RPIYOP 191
 |||||
 Db 199 RPIYOP 205

RESULT 30
 VB1_CLVK STANDARD; PRT; 298 AA.
 AC P14971;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE B1 protein (33.7 kDa protein).
 GN BCL1.
 OS Cassava latent virus (strain Nigerian).
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxID=10819;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90174930; PubMed=2308831;
 RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;
 RT "Nucleotide sequence of the infectious cloned DNA components of
 RT African cassava mosaic virus (Nigerian strain).";
 RL Nucleic Acids Res. 18:197-198(1990).
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES B1 PROTEIN FAMILY.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X17096; CAA34955.1; -
 DR PIR; S07596; S07596.
 DR InterPro; IPR000211; Gemini_B1.
 DR Pfam; PF00845; Gemini_B1; 1.
 SO SEQUENCE 298 AA; 33648 MW; 87C5BCE912519526 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 298;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 RPIYOP 191
 |||||
 Db 199 RPIYOP 205

Search completed: June 18, 2002, 14:32:26
 Job time: 214 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:29:27 ; Search time 26.53 Seconds
(without alignments)
1806.242 Million cell updates/sec

Title: US-09-852-845-2
Perfect score: 277
Sequence: 1 MCVGARRLRGPCFCAALLLLG.....SFRPTQEQADAHSLAKI 277

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database :

SPTREMBL_19:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	6.1	267	6	002764
2	9	3.2	2126	11	0920T6
3	8	2.9	109	11	0920X4
4	8	2.9	151	4	090F74
5	8	2.9	162	11	09CWE9
6	8	2.9	162	16	051707
7	8	2.9	185	7	09NFG2
8	8	2.9	191	4	09H7A9
9	8	2.9	199	16	098KM8
10	8	2.9	204	5	09NFD4
11	8	2.9	208	11	09D5A9
12	8	2.9	215	5	020614
13	8	2.9	236	7	031625
14	8	2.9	236	7	031359
15	8	2.9	250	7	031150
16	8	2.9	250	11	09QWV1

17	8	2.9	264	2	09X647	09X647 aeromonas h
18	8	2.9	282	4	09NPF0	09NPF0 homo sapien
19	8	2.9	306	2	09FDR4	09FDR4 straphylococ
20	8	2.9	315	16	099UT7	099UT7 staphylococ
21	8	2.9	329	10	043324	043324 populus x c
22	8	2.9	432	2	093J03	093J03 streptomyc
23	8	2.9	443	16	09HW78	09HW78 pseudomonas
24	8	2.9	473	11	09CY76	09CY76 mus musculu
25	8	2.9	473	16	005295	005295 mycobacteri
26	8	2.9	476	16	050017	050017 mycobacteri
27	8	2.9	513	16	097097	097097 streptococ
28	8	2.9	576	11	09JLT2	09JLT2 mus musculu
29	8	2.9	621	4	09P264	09P264 homo sapien
30	8	2.9	768	4	060279	060279 homo sapien
31	8	2.9	852	4	09H956	09H956 homo sapien
32	8	2.9	1031	10	065500	065500 arabidopsis
33	8	2.9	45	11	09ET76	09ET76 mus musculu
34	7	2.5	47	10	09FSP6	09FSP6 oryza sativ
35	7	2.5	52	8	036274	036274 zea mays (m
36	7	2.5	53	4	096IX8	096IX8 homo sapien
37	7	2.5	88	2	P71190	P71190 escherichia
38	7	2.5	93	16	09RZ65	09RZ65 deinococcus
39	7	2.5	100	12	091FS4	091FS4 chilo iride
40	7	2.5	103	16	09RWM3	09RWM3 deinococcus
41	7	2.5	105	11	0920X5	0920X5 mus musculu
42	7	2.5	105	11	091VE7	091VE7 mus musculu
43	7	2.5	113	2	045273	045273 bradyrhizob
44	7	2.5	114	5	095Q94	095Q94 caenorhabdi
45	7	2.5	115	13	090Y43	090Y43 osteoglossu
46	7	2.5	116	10	09ZSJ6	09ZSJ6 arabidopsis
47	7	2.5	116	16	09XIV2	09XIV2 thermotoga
48	7	2.5	129	9	094MT2	094MT2 bacterioph
49	7	2.5	133	16	P74742	P74742 synechocyst
50	7	2.5	139	16	09JR37	09JR37 neisseria m

ALIGNMENTS

RESULT 1

ID 002764 PRELIMINARY; PRT; 267 AA.

AC 002764;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)

DE OX40 PRECURSOR (FRAGMENT).

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxId=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CHB:HM;

RA Isono T., Seto A.;

RT "Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed T cell lines."

RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB003911; BAA20059.1; -.

DR HSSP; P25942; 1CDF.

DR InterPro; IPR01368; TNFR_c6.

DR Pfam; PF00020; TNFR_c6; 3.

DR ProDom; PD000771; TNFR_c6; 1.

DR SMART; SM00208; TNFR_3.

DR PROSITE; PS00852; TNFR_NGFR_1; 2.

DR PROSITE; PS0050; TNFR_NGFR_2; 2.

KW Signal.

FT NON_TER

FT SIGNAL

FT CHAIN

SO SEQUENCE

267 AA; 267 MW; ABB4CD3173C9500B CRC64;

<1 18 POTENTIAL.

OX40

Query Match 6.1%; Score 17; DB 6; Length 267;
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 254 PGSGSFRPIOEQADA 270
 DB 244 PGSGSFRPIOEQADA 260

RESULT 2
 ID 0920T6 PRELIMINARY; PRT; 2126 AA.
 AC 0920T6;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE POLYCYSTIC KIDNEY DISEASE AND RECEPTOR FOR EGG JELLY RELATED
 DE PROTEIN.
 GN PKDREJ.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=99138702; PubMed=9949214;
 RA Hughes J., Ward C.J., Aspinwall R., Butler R., Harris P.C.;
 RT "Identification of a human homologue of the sea urchin receptor for
 egg jelly: a polycystic kidney disease-like protein.";
 RL Hum. Mol. Genet. 8:543-549(1999).
 DR EMBL; AF16455; AAD18022.1; .
 DR MGD; MGI:1338786; PKDreJ.
 DR InterPro; IPR000636; Cation_chan_non_119.
 DR InterPro; IPR002111; Cat_channel_TrpL.
 DR InterPro; IPR001024; LH2.
 DR InterPro; IPR002033; PKD_cys_rich.
 DR InterPro; IPR002859; REJ.
 DR Pfam; PF00520; Ion_trans; 1.
 DR Pfam; PF01477; PLAT; 1.
 DR Pfam; PF02010; REJ; 1.
 DR SMART; SM00303; GPS; 1.
 DR SMART; SM00308; LH2; 1.
 KW Receptor.
 SQ SEQUENCE 2126 AA; 241389 MW; A0CEDA0D8219A84 CRC64;

Query Match 3.2%; Score 9; DB 11; Length 2126;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 ALLLGLGL 23
 DB 6 ALLLGLGL 14

RESULT 3
 ID 0920X4 PRELIMINARY; PRT; 109 AA.
 AC 0920X4;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE CAHELICIDIN (FRAGMENT).
 GN CRAMP.
 OS Mus spicilegus (Steppe mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA SPRIN=2BN.
 RA Liu Y., Kilano T., Koide T., Shirosaki T., Moriwaki K., Saitou N.;
 RT "Conspecific Differences among Gene Genealogies of 21 Nuclear Genes of

RT Five Mus musculus subspecies.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB039073; BAB68597.1; .
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 109 AA; 12230 MW; 8FE0162551AA477C CRC64;

Query Match 2.9%; Score 8; DB 11; Length 109;
 Best Local Similarity 100.0%; Pred. No. 6.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGLGL 23
 DB 16 LLLGLGL 23

RESULT 4
 ID 09UF74 PRELIMINARY; PRT; 151 AA.
 AC 09UF74;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE HYPOTHETICAL 16.6 KDA PROTEIN (FRAGMENT).
 GN DKE2P434N1535.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE=TESTIS;
 RA Poultka A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL133575; CAB63722.1; .
 KW Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 151 AA; 16584 MW; 8092E652B311821 CRC64;

Query Match 2.9%; Score 8; DB 4; Length 151;
 Best Local Similarity 100.0%; Pred. No. 8.9;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 LGSTVTVG 28
 DB 35 LGSTVTVG 42

RESULT 5
 ID 09CWE9 PRELIMINARY; PRT; 162 AA.
 AC 09CWE9;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE 241014IK03RIK PROTEIN.
 GN 241014IK03RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaoka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Sakurai L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Blake J., Boffelli D., Fujuno M., Aono H., Balderelli R., Barsh G.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontuski S.,
 RA Hayashizaki Y.,
 RT "Functional annotation of a full-length mouse cDNA collection.",
 RL Nature 409:685-690(2001).
 DR EMBL: AK010803; BAB27191.1; -;
 DR MGD: MGI:1915216; 2410141K03Rik.
 DR InterPro: IPR001878; Znf_CCHC.
 DR Pfam: PF00098; Zf-CCHC; 1.
 DR SMART: SM00343; Znf_C2HC; 1.
 KW Zinc-finger.
 SQ SEQUENCE 162 AA; 17758 MW; 2CCA4888DC57B78E CRC64;

Query Match 2.9%; Score 8; DB 11; Length 162;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LGLVLGL 23
 DB 144 LGLVLGL 151

RESULT 6
 ID 051707 PRELIMINARY; PRT; 162 AA.
 AC 051707;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE COLICIN V PRODUCTION PROTEIN, PUTATIVE.
 GN BB0766.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson S., Hanson M.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Bowman J.,
 RA Ueberback T., Wathey L., McDonald L., Artach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi."
 RL Nature 380:580-586(1997).
 DR EMBL: AE001176; AAC67114.1; -;
 DR TIGR: BB0766;
 DR InterPro: IPR003825; Colicin_V.
 DR Pfam: PF02674; Colicin_V; 1.
 KW Complete proteome.
 SQ SEQUENCE 162 AA; 18715 MW; 7FFA560D3EBE4201 CRC64;

Query Match 2.9%; Score 8; DB 16; Length 162;
 Best Local Similarity 100.0%; Pred. No. 9.4;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 221 LGLVLGL 228
 DB 111111111

DB 107 LGLVLGL 114
 RESULT 7
 ID 09NF02 PRELIMINARY; PRT; 185 AA.
 AC 09NF02;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE HYPOTHETICAL 21.7 KDA PROTEIN (FRAGMENT).
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3D7A;
 RX MEDLINE=97008413; PubMed=8855557;
 RA Alano P., Silvestrini F., Roca L.;
 RT "Structure and polymorphism of the upstream region of the pfg 27/25
 RT gene, transcriptionally regulated in gametocytogenesis of Plasmodium
 RT falciparum."
 RL Mol. Biochem. Parasitol. 79:207-217(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3D7A;
 RX MEDLINE=20520959; PubMed=11071280;
 RA Sallicandro P., Paglia M.G., Hashim S.O., Silvestrini F., Picci L.,
 RA Gentile M., Mulaa F., Alano P.;
 RT "Repetitive sequences upstream of the pfg27/25 gene determine
 RT polymorphism in laboratory and natural lines of Plasmodium
 RT falciparum."
 RL Mol. Biochem. Parasitol. 110:247-257(2000).
 DR EMBL: AJ271108; CAB93664.1; -;
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 185 AA; 21653 MW; 774285C81B10A3D0 CRC64;

Query Match 2.9%; Score 8; DB 5; Length 185;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 215 VAILIGLG 222
 DB 31 VAILIGLG 38

RESULT 8
 ID 09H7A9 PRELIMINARY; PRT; 191 AA.
 AC 09H7A9;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE CDNA: FLJ21104 FIS, CLONE CAS04958.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,
 RA Ohashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,
 RA Isogai T., Sugano S.;
 RT "NEDO human cDNA sequencing project."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AK024757; BAB14988.1; -;
 SQ SEQUENCE 191 AA; 20917 MW; COEBB49678F36E0B CRC64;

```

Query Match      2.9%; Score 8; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 FSPGDNOA 140
    |||||||
DB 59 FSPGDNOA 66

RESULT 9
O98KM8 PRELIMINARY; PRT: 199 AA.
AC O98KM8:
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE MLR1403 PROTEIN.
GN MLR1403.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=1121968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idegawa K., Ishikawa A., Kawasaki K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL; AP002997; BAB48786.1; -
KM Complete proteome.
SQ SEQUENCE 199 AA; 22658 MW; 2AF1DECDAF29AB0 CRC64;

Query Match      2.9%; Score 8; DB 16; Length 199;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 AAILGL 223
    |||||||
DB 125 AAILGL 132

RESULT 10
O9NFU4 PRELIMINARY; PRT: 204 AA.
AC O9NFU4:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYOTHEFTICAL 23 8 KDA PROTEIN (FRAGMENT).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20520959; PubMed=11071280;
RX Salicandro P., Paglia M.G., Hashim S.O., Silvestrini F., Picci L.,
RX Gentile M., Mula F., Alano P.;
RT "Repetitive sequences upstream of the pfq27/25 gene determine
RT polymorphism in laboratory and natural lines of Plasmodium
RT falciparum."
RL Mol. Biochem. Parasitol. 110:247-257(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97008413; PubMed=8855557;
RA Alano P., Silvestrini F., Roca L.;
RT "Structure and polymorphism of the upstream region of the pfq 27/25

```

```

RT gene, transcriptionally regulated in gametocytogenesis of Plasmodium
RT falciparum.";
RL Mol. Biochem. Parasitol. 79:207-217(1996).
DR EMBL; AJ271088; CAB93662.1; -
KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 204 AA; 23806 MW; 27145AFB71EDEF731 CRC64;

Query Match      2.9%; Score 8; DB 5; Length 204;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 VAILGLG 222
    |||||||
DB 50 VAILGLG 57

RESULT 11
O9D5A9 PRELIMINARY; PRT: 208 AA.
AC O9D5A9:
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 4930474F22RIK PROTEIN.
GN 4930474F22RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=TESTIS;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Queckenbush J.,
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boilelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL; AK015573; BAB29896.1; -
DR HSSP; P00669; IBSR.
DR MGD; MGI:1922269; 4930474F22RIK.
DR InterPro; IPR001427; RNaseA.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_Pc; 1.
SQ SEQUENCE 208 AA; 23407 MW; 383F776927F6067C CRC64;

Query Match      2.9%; Score 8; DB 11; Length 208;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGLGL 23
    |||||||
DB 14 LLLGLGL 21

```

RESULT 12
Q20614 PRELIMINARY; PRT: 215 AA.
AC Q20614;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE F49E12.7 PROTEIN.
GN F49E12.7.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Thomas K.;
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=99069613; PubMed=9851916;
RA none;
RT "Genome sequence of the nematode C.elegans: A platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; Z66520; CAA91386.1; -;
SQ SEQUENCE 215 AA; 24861 MW; 23352PFD0969A84C8 CRC64;

Query Match 2.9%; Score 8; DB 5; Length 215;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 230 PLATLAL 237
Db 25 PLATLAL 32

RESULT 13
Q31625 PRELIMINARY; PRT: 236 AA.
AC Q31625;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC CLASS II ALPHA CHAIN.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011091; PubMed=8406613;
RA Sultmann H., Mayer W.E., Figueroa F., O'Huigin C., Klein J.;
RT "Zebrafish MHC class II alpha chain-encoding genes: polymorphism,
RT expression, and function."
DE Immunogenetics 38:408-420(1993).
GN H2-OA OR H-2OA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-B10.M; TISSUE=SPLEEN;
RX MEDLINE=92364550; PubMed=1354242;
RA Karlsson L., Peterson P.A.;
RT "The alpha chain gene of H-2O has an unexpected location in the MHC."
RL J. Exp. Med. 176:477-483(1992).
DR EMBL; M95514; AAB46387.1; -;
DR HSSP; P01903; 1A6A.
DR MGD; MGI:95924; H2-Oa.
DR InterPro; IPR003597; Ig_C1.
SQ SEQUENCE 236 AA; 26205 MW; 9E1F01C034C90B20 CRC64;

Query Match 2.9%; Score 8; DB 7; Length 236;

Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 GLVGLLG 229
Db 214 GLVGLLG 221

RESULT 14
Q31359 PRELIMINARY; PRT: 236 AA.
AC Q31359;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC CLASS II ALPHA CHAIN.
OS Brachydanio rerio (zebrafish) (Zebra danio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
OC Cypriniformes; Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011091; PubMed=8406613;
RA Sultmann H., Mayer W.E., Figueroa F., O'Huigin C., Klein J.;
RT "Zebrafish MHC class II alpha chain-encoding genes: polymorphism,
RT expression, and function."
DE Immunogenetics 38:408-420(1993).
GN H2-OA OR H-2OA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-B10.M; TISSUE=SPLEEN;
RX MEDLINE=92364550; PubMed=1354242;
RA Karlsson L., Peterson P.A.;
RT "The alpha chain gene of H-2O has an unexpected location in the MHC."
RL J. Exp. Med. 176:477-483(1992).
DR EMBL; M95514; AAB46387.1; -;
DR HSSP; P01903; 1A6A.
DR MGD; MGI:95924; H2-Oa.
DR InterPro; IPR003597; Ig_C1.
SQ SEQUENCE 236 AA; 26136 MW; 3780A1609ACBE285 CRC64;

Query Match 2.9%; Score 8; DB 7; Length 236;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 222 GLVGLLG 229
Db 214 GLVGLLG 221

RESULT 15
Q31150 PRELIMINARY; PRT: 250 AA.
AC Q31150;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MHC CLASS II ALPHA CHAIN PRECURSOR.
GN H2-OA OR H-2OA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN-B10.M; TISSUE=SPLEEN;
RX MEDLINE=92364550; PubMed=1354242;
RA Karlsson L., Peterson P.A.;
RT "The alpha chain gene of H-2O has an unexpected location in the MHC."
RL J. Exp. Med. 176:477-483(1992).
DR EMBL; M95514; AAB46387.1; -;
DR HSSP; P01903; 1A6A.
DR MGD; MGI:95924; H2-Oa.
DR InterPro; IPR003597; Ig_C1.

```

DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001003; MHC_II_alpha.
DR Pfam: PF00047; Ig_1.
DR Pfam: PF00993; MHC_II_alpha; 1.
DR SMART: SM00407; IgC1; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
KW Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 250 MHC CLASS II ALPHA CHAIN.
SQ SEQUENCE 250 AA; 28182 MW; C20A397B2EFA2004 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 7; Length 250;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 GGLVGL 227
DB 222 GGLVGL 229

RESULT 16
Q9QWV1 PRELIMINARY; PRT; 250 AA.
ID 09QWV1
AC 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE H2-O ALPHA (HISTOCOMPATIBILITY 2, O REGION ALPHA LOCUS).
GN H2-OALPHA OR H2-OA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_Taxid=10090;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN-129SVJ;
RA Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,
RA Hall J., Lasky S., Hood L.;
RT "Sequence of the mouse major histocompatibility locus class II
RT region."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
RP SEQUENCE FROM N.A.
RC STRAIN-C57BL/6J; TISSUE=URINARY BLADDER;
RX MEDLINE=21085660; PUBMED=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Bersh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombaerts P.,
RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,
RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection."
RL Nature 409:685-690(2001).
DR EMBL: AF100956; AAC69906.1; -
DR EMBL: AK020594; BAB32142.1; -
DR HSRF: P01903; 1A6A.
DR MGD: MGI:95924; H2-Oa.
DR InterPro: IPR003597; Ig_c1.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR001003; MHC_II_alpha.

```

```

DR Pfam: PF00047; Ig_1.
DR Pfam: PF00993; MHC_II_alpha; 1.
DR SMART: SM00407; IgC1; 1.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 250 AA; 28166 MW; 98BCF2E8926076A1 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 11; Length 250;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 GGLVGL 227
DB 222 GGLVGL 229

RESULT 17
Q9X647 PRELIMINARY; PRT; 264 AA.
ID 09X647
AC 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DE 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE HYPOTHETICAL 28.2 KDA PROTEIN.
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;
OC Aeromonas.
OX NCBI_Taxid=644;
RN 11
RP SEQUENCE FROM N.A.
RA Aguilar A., Merino S., Noguera M.M., Regue M., Tomas J.M.;
RT "Two genes from the capsule of Aeromonas hydrophila (serogroup O:34)
RT confer serum resistance to Escherichia coli K-12 strains."
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF131869; AAD34732.1; -
DR InterPro: IPR000326; PA_PTPase.
DR Pfam: PF01569; PAP2; 1.
KW Hypothetical protein.
SQ SEQUENCE 264 AA; 28163 MW; 8953984BCAC64FD6 CRC64;

Query Match
Best Local Similarity 100.0%; Score 8; DB 2; Length 264;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 PCAALL 19
DB 18 PCAALL 25

RESULT 18
Q9NPFO PRELIMINARY; PRT; 282 AA.
ID 09NPFO
AC 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE 8D6 ANTIGEN (HYPOTHETICAL 29.0 KDA PROTEIN).
GN DKFZP564O1762.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN 11
RP SEQUENCE FROM N.A.
RA Carim L., Estivill X., Escarceller M., Sumoy L.;
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN 121
RP SEQUENCE FROM N.A.
RA Aufray C., Ansoorge W., Ballabio A., Estivill X., Gibson K.,
RA Lehnach H., Poustka A., Lundberg J.;
RT "The European IMAGE consortium for integrated Molecular analysis of
RT human gene transcripts."

```

```

RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193707; PubMed=10727470;
RA Li L., Zhang X., Kovacic S., Long A.J., Bourque K., Wood C.R.,
RA Choi Y.S.;
RT "Identification of a human follicular dendritic cell molecule that
RT stimulates germinal center B cell growth.";
RL J. Exp. Med. 191:1077-1084(2000).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Blum H., Baueersachs S., Mewes H.W., Gassenhuber J., Wiemann S.;
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE=KIDNEY ADENOCARCINOMA;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN, PRIMITIVE NEUROECTODERMAL;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL365455; CAB97010.1; -;
DR EMBL; AF161254; AAF61850.1; -;
DR EMBL; AL136652; CAB66587.1; -;
DR EMBL; BC000668; AAH00668.1; -;
DR EMBL; BC007083; AAH07083.1; -;
DR HSSP; Q07954; ICR8.
DR InterPro: IPR002172; LDL_recept_A.
DR Pfam; PF00057; ldl_recept_a; 2.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM00192; LDLra_2.
DR PROSITE; PS01209; LDLRA_1; 2.
DR PROSITE; PS50066; LDLRA_2; 2.
KW Glycoprotein.
SQ SEQUENCE 282 AA; 28991 MW; 59E172986B220E4F CRC64;

Query Match 2.9%; Score 8; DB 4; Length 282;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 LLLGLGL 23
Db 22 LLLGLGL 29

RESULT 19
O9FDT4 PRELIMINARY; PRT; 306 AA.
AC O9FDT4;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE EXFOLIATIVE TOXIN A.
GN SHETA.
OS Staphylococcus hyicus.
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=1284;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=P-1;
RX MEDLINE=20327593; PubMed=10869091;
RA Watanabe T., Sato H., Hatakeyama Y., Matsuzawa T., Kawai M.,
RA Aizawa C., Danbara H., Maehara N.;
RT "Cloning of the gene coding for Staphylococcus hyicus exfoliative
RT toxin A and its expression in Escherichia coli.";
RL J. Bacteriol. 182:4101-4103(2000).
DR EMBL; AB036768; BAB08178.1; -.
SQ SEQUENCE 306 AA; 34379 MW; 60B7EDF3677ACDDF CRC64;

```

```

Query Match 2.9%; Score 8; DB 2; Length 306;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 222 GLVGLGLG 229
Db 12 GLVGLGLG 19

RESULT 20
O99UT7 PRELIMINARY; PRT; 315 AA.
AC O99UT7;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HYPOTHETICAL PROTEIN SA1016 (HYPOTHETICAL PROTEIN SAV1173).
GN SA1016 OR SAV1173.
OS Staphylococcus aureus (strain N315), and
OC Staphylococcus aureus (strain Mu50).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Bacillus/Staphylococcus group; Staphylococcus.
OX NCBI_TaxID=158879, 158878;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain N315), and S.aureus (strain Mu50);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hiraoka H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003132; BAB42268.1; -.
DR EMBL; AP003361; BAB57335.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 315 AA; 35236 MW; 74B814BDE7243139 CRC64;

Query Match 2.9%; Score 8; DB 16; Length 315;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 222 GLVGLGLG 229
Db 12 GLVGLGLG 19

RESULT 21
O43324 PRELIMINARY; PRT; 329 AA.
AC O43324;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE MAJOR STORAGE PROTEIN;
OS Populus x canadensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids I; Malpighiales; Salicaceae; Populus.
OX NCBI_TaxID=3690;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92003681; PubMed=1912491;
RA Clausen S., Apel K.;
RT "Seasonal changes in the concentration of the major storage protein
RT and its mRNA in xylem ray cells of poplar trees.";

```

RL Plant Mol. Biol. 17:669-678(1991).
 DR EMBL: S59422; AAB20113.2; -;
 SQ SEQUENCE 329 AA; 36055 MW; 875C867A15042204 CRC64;

Query Match
 Best Local Similarity 2.9%; Score 8; DB 10; Length 329;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 AALLLGL 21
 |||||
 Db 7 AALLLGL 14

RESULT 22
 O93J03 PRELIMINARY; PRT; 432 AA.
 ID O93J03:
 AC O93J03:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DE PUTATIVE INTEGRAL MEMBRANE PROTEIN.
 GN SCBAC25F8.09.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2):
 RA Seeger K., Harris D.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2):
 RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2):
 RX MEDLINE=97000351; PubMed=8843436;
 RA Redenbach M., Kleiser H.M., Denaplatte D., Elchner A., Cullum J.,
 RA Kinasch H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 DR EMBL: AL592126; CAC42144.1; -;
 SQ SEQUENCE 432 AA; 43516 MW; DC222112875091B7 CRC64;

Query Match
 Best Local Similarity 2.9%; Score 8; DB 2; Length 432;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGL 23
 |||||
 Db 70 LLLGL 77

RESULT 23
 O9HW78 PRELIMINARY; PRT; 443 AA.
 ID O9HW78:
 AC O9HW78:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DE HYPOTHEICAL PROTEIN PA4323.
 GN PA4323.
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 OX NCBI_TaxID=287;
 RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-ATCC 15692 / PA01:
 RX MEDLINE=20437337; PubMed=10984043;
 RA Stover C.K., Pham X.-O.T., Ervin A.L., Mizoguchi S.D., Warrenner P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wedman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lablitz K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 opportunistic pathogen.";
 RL Nature 406:959-964(2000).
 DR EMBL: AE004848; AAG07711.1; -;
 DR InterPro: IPR002881; DUF58.
 DR InterPro: IPR002035; vWFA.
 DR Pfam: PF01882; DUF58; 1.
 DR SMART: SM00327; vWA; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 443 AA; 50359 MW; A3814456A5D5EBA8 CRC64;

Query Match
 Best Local Similarity 2.9%; Score 8; DB 16; Length 443;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 AALLLGL 21
 |||||
 Db 44 AALLLGL 51

RESULT 24
 O9CY76 PRELIMINARY; PRT; 473 AA.
 ID O9CY76:
 AC O9CY76:
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DE 5730589L02RIK PROTEIN.
 GN 5730589L02RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE=EMBRYO.
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamane A.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Queckenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyokawa K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL: AK019981; BAB31950.1; -;
 DR GDB: MGI:1924832; 5730589L02RIK.
 SQ SEQUENCE 473 AA; 53504 MW; CE6F8E93C3D01C4F CRC64;

Query Match
 2.9%; Score 8; DB 11; Length 473;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LGIGLVIG 226
DB 441 LGIGLVIG 448

RESULT 25

ID 005295 PRELIMINARY; PRT; 473 AA.

AC 005295;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HYPOHETICAL 49.5 KDA PROTEIN.
GN PADD36 OR RV1193 OR MTC1364.05.
OS Mycobacterium tuberculosis.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1773;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=H37RV;
RX MEDLINE=98295987; PubMed=9634230;
RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
RA Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
RT "Deciphering the biology of Mycobacterium tuberculosis from the
RT complete genome sequence."
RL Nature 393:537-544(1998).
DR EMBL: Z93777; CAB07836.1; -.
DR HSSP: P08659; ILCI.
DR Tuberculist: RV1193; -.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR003015; HLH_Myc.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP_BINDING; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Hypothetical protein: Complete proteome.
SQ SEQUENCE 473 AA; 49520 MW; 39ECC2B0D02BAD3D CRC64;

Query Match 2.9%; Score 8; DB 16; Length 473;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVIGLIG 229
DB 184 GLVIGLIG 191

RESULT 26

ID 050017 PRELIMINARY; PRT; 476 AA.

AC 050017;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE XCIC (ACTV-COA SYNTHASE).
GN XCIC OR ML1051.
OS Mycobacterium lepreae.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OX NCBI_TaxID=1769;
RN [1]
RP SEQUENCE FROM N.A.

RA Smith D.R., Robison K.;
RL submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=TN;
RX MEDLINE=21128732; PubMed=11234002;
RA Cole S.T., Eiglmeyer K., Parkhill J., James K.D., Thomson N.R.,
RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,
RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,
RA Davies R.M., Devlin K., Duthoy S., Felwell T., Fraser A., Hamlin N.,
RA Holroyd S., Hornsby T., Jagels K., Lacroix C., McLean J., Moule S.,
RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,
RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,
RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,
RA Barrell B.G.;
RT "Massive gene decay in the leprosy bacillus."
RL Nature 408:1007-1011(2001).
DR EMBL: U15181; AAA62961.1; -.
DR EMBL: AL583920; CAC1432.1; -.
DR HSSP: P08659; ILCI.
DR Leproma: ML1051; -.
DR InterPro: IPR000873; AMP-bind.
DR InterPro: IPR003015; HLH_Myc.
DR Pfam: PF00501; AMP-binding; 1.
DR PRINTS: PR00154; AMPBINDING.
DR PROSITE: PS00455; AMP_BINDING; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 476 AA; 50130 MW; 4F8DEED72059E66E CRC64;

Query Match 2.9%; Score 8; DB 16; Length 476;

Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVIGLIG 229
DB 187 GLVIGLIG 194

RESULT 27

ID 097097 PRELIMINARY; PRT; 513 AA.

AC 097097;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SODIUM: Solute symporter family protein.
GN SPI328.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouir H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
RT pneumoniae."
RL Science 293:498-506(2001).
DR EMBL: AE007431; AAK75426.1; -.
DR TIGR: SPI328; -.
DR InterPro: IPR001734; Na_solut_sympo.
DR Pfam: PF00474; SSF; 1.
DR PROSITE: PS00456; NA_solut_symp_1; UNKNOWN_1.

DR PROSITE: PS50283; NA_SOLUT_SYMP_3; 1.
 KW Complete proteome.
 SQ SEQUENCE 513 AA; 55768 MW; D9E9CE6A9A8417E7 CRC64;

Query Match 2.9%; Score 8; DB 16; Length 513;
 Best Local Similarity 100.0%; Pred. No. 25;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 GLVLGLG 229
 |||||
 DB 414 GLVLGLG 421

RESULT 28

ID 09JLT2 PRELIMINARY; PRT; 576 AA.
 AC 09JLT2:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE TRHHAALASE (EC 3.2.1.28) (2210412M19RIK PROTEIN).
 GN TRH OR 2210412M19RIK.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-DDY; TISSUE=INTESTINAL MUCOSA;
 RA Ohba T., Kudo N., Ariyasu H., Yanai Y., Takeuchi M., Ikegami H.,
 RL Kurimoto M.;
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-C57BL/6J; TISSUE=STOMACH;
 RA MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinsawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
 RA Aitawa K., Itawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochia H.,
 RA Kuehl P., Lewis S., Matsuo S., Nikaido I., Peesle G., Quackenbush J.,
 RA Schirml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.F.,
 RA Guetlich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilting L.,
 RA Wyszewski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,
 RA Hayshtizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN EMBL; AF136944; AA61430.1; -
 DR EMBL; AK008912; BAB25963.1; -
 DR MGD; MGI:1926230; Treh.
 DR InterPro: IPR001661; Trehalase.
 DR Pfam; PF01204; Trehalase; 1.
 DR PRINTS; PRO0744; GLHYDRLASE37.
 DR PROSITE; PS00927; TREHHAALASE_1; 1.
 DR PROSITE; PS00928; TREHHAALASE_2; 1.
 KW Hydrolase; Glycosidase.
 SQ SEQUENCE 576 AA; 65401 MW; 53CDA6A10511520E CRC64;

Query Match 2.9%; Score 8; DB 11; Length 576;
 Best Local Similarity 100.0%; Pred. No. 28;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLGLGL 23
 |||||
 DB 8 LLLGLGL 15

RESULT 29

ID 09P264 PRELIMINARY; PRT; 621 AA.
 AC 09P264:
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE KIA1464 PROTEIN (FRAGMENT).
 GN KIA1464.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=20277482; PubMed=10819331;
 RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human
 genes. XVII. The complete sequences of 100 new cDNA clones from brain
 which code for large proteins in vitro.";
 RL DNA Res. 7:143-150(2000).
 DR EMBL; AB040897; BAA95988.1; -
 DR InterPro: IPR003877; SPRY.
 DR InterPro: IPR003878; SPRY_domain.
 DR Pfam; PF00622; SPRY; 1.
 DR SMART; SM00449; SPRY; 1.
 FT NON_TER 1

SQ SEQUENCE 621 AA; 67385 MW; DBC285CDB9CFD40C CRC64;

Query Match 2.9%; Score 8; DB 4; Length 621;
 Best Local Similarity 100.0%; Pred. No. 30;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 TPIOEQA 268
 |||||
 DB 284 TPIOEQA 291

RESULT 30

ID 060279 PRELIMINARY; PRT; 768 AA.
 AC 060279:
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE KIA0527 PROTEIN (FRAGMENT).
 GN KIA0527.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_Taxid=9606;

RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRIN;
 RA MEDLINE=98290545; PubMed=9628581;
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
 RA Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 The complete sequences of 100 new cDNA clones from brain which can
 code for large proteins in vitro.";
 RL DNA Res. 5:31-39(1998).
 DR EMBL; AB011099; BAA25453.1; -
 DR InterPro: IPR000538; Link.
 DR InterPro: IPR000435; Sush1_SCR_CCP.
 DR Pfam; PF00084; sush1; 1.
 DR SMART; SM00032; CCP; 1.
 DR SMART; SM00445; LINK; 1.

FT NON_TER 1 1
SQ SEQUENCE 768 AA; 82680 MM; B97A932B44883536 CRC64;

Query Match 2.9%; Score 8; DB 4; Length 768;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 AALLLGL 21
|||||||
Db 161 AALLLGL 168

Search completed: June 18, 2002, 14:33:01
Job time: 214 sec

THIS PAGE BLANK (USPTO)

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:25:22 ; Search time 13.13 Seconds
(without alignments)
515.300 Million cell updates/sec

Title: US-09-852-845-2

Perfect score: 277

Sequence: 1 MCVGARRLGRGPCALLLLG.....SFRTPIQEQADAHSTLAKI 277

Scoring table:

OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size: 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep.*
4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep.*
5: /cgn2_6/ptodata/2/1aa/PCUS_COMB.pep.*
6: /cgn2_6/ptodata/2/1aa/backfilltest.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	277	100.0	277	2	US-08-147-784-2	Sequence 2, Appli
2	277	100.0	277	4	US-08-195-967-2	Sequence 2, Appli
3	277	100.0	277	4	US-09-006-353A-12	Sequence 12, Appli
4	277	100.0	277	4	US-08-472-940-2	Sequence 2, Appli
5	56	20.2	56	4	US-08-866-545-10	Sequence 10, Appli
6	12	4.3	41	1	US-08-050-319B-44	Sequence 44, Appli
7	12	4.3	41	2	US-08-465-982-44	Sequence 44, Appli
8	12	4.3	133	4	US-08-468-560C-8	Sequence 8, Appli
9	12	4.3	133	2	US-08-219-237B-8	Sequence 8, Appli
10	12	4.3	140	4	US-08-477-347-17	Sequence 17, Appli
11	12	4.3	140	8	US-08-476-862-8	Sequence 8, Appli
12	12	4.3	205	3	US-08-974-022-51	Sequence 51, Appli
13	12	4.3	205	4	US-08-795-445A-51	Sequence 51, Appli
14	12	4.3	205	4	US-08-795-447A-51	Sequence 51, Appli
15	12	4.3	205	4	US-08-974-166-51	Sequence 51, Appli
16	12	4.3	206	1	US-08-795-446B-51	Sequence 51, Appli
17	12	4.3	206	1	US-08-097-827-7	Sequence 7, Appli
18	12	4.3	206	1	US-08-494-574-7	Sequence 7, Appli
19	12	4.3	438	1	US-08-097-827-11	Sequence 11, Appli
20	12	4.3	438	1	US-08-494-574-11	Sequence 11, Appli
21	9	3.2	625	3	US-08-996-139-15	Sequence 15, Appli
22	9	3.2	625	3	US-08-995-659-15	Sequence 15, Appli
23	7	2.5	625	4	US-09-215-649A-15	Sequence 15, Appli
24	7	2.5	30	4	US-09-105-390-20	Sequence 20, Appli
25	7	2.5	105	4	US-09-124-671-17	Sequence 17, Appli
26	7	2.5	109	4	US-09-124-671-19	Sequence 19, Appli
27	7	2.5	109	4	US-09-124-671-21	Sequence 21, Appli

28	7	2.5	115	4	US-09-124-671-13	Sequence 13, Appli
29	7	2.5	115	4	US-09-124-671-15	Sequence 15, Appli
30	7	2.5	128	1	US-08-478-039-110	Sequence 110, App
31	7	2.5	128	1	US-08-476-349A-110	Sequence 110, App
32	7	2.5	128	4	US-08-523-894-4	Sequence 4, Appli
33	7	2.5	134	4	US-09-124-671-34	Sequence 34, Appli
34	7	2.5	144	2	US-08-341-843B-39	Sequence 39, Appli
35	7	2.5	144	2	US-08-427-497E-44	Sequence 44, Appli
36	7	2.5	209	2	US-08-827-279-1	Sequence 1, Appli
37	7	2.5	233	4	US-08-523-894-6	Sequence 6, Appli
38	7	2.5	243	4	US-09-188-930-295	Sequence 295, App
39	7	2.5	261	2	US-08-484-905-111	Sequence 111, App
40	7	2.5	261	3	US-08-481-985B-111	Sequence 111, App
41	7	2.5	261	4	US-08-370-476-111	Sequence 12, Appli
42	7	2.5	327	1	US-08-375-962B-12	Sequence 12, Appli
43	7	2.5	327	2	US-08-562-114B-12	Sequence 12, Appli
44	7	2.5	327	4	US-08-729-594A-12	Sequence 12, Appli
45	7	2.5	335	2	US-08-875-062-3	Sequence 3, Appli
46	7	2.5	336	4	US-09-105-390-52	Sequence 52, Appli
47	7	2.5	406	4	US-08-506-296B-5	Sequence 5, Appli
48	7	2.5	415	1	US-08-110-286A-2	Sequence 2, Appli
49	7	2.5	415	1	US-08-110-286A-6	Sequence 6, Appli
50	7	2.5	415	4	US-08-981-109B-10	Sequence 10, Appli

ALIGNMENTS

RESULT 1
US-08-147-784-2
; Sequence 2, Application US/08147784
; Patent No. 5821332
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Buck, David
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/147,784
; FILING DATE: 03-NOV-1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-220
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO. 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-147-784-2
Query Match 100.0%; Score 277; DB 2; Length 277;
Best Local Similarity 100.0%; Pred. No. 1,4e-260;

Matches 277: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCVGARRLGRPCALLLLGLSTVTLGHCVDTPYPSNDRCHCPCPGNGMVSRCRSQ 60
Db 1 MCVGARRLGRPCALLLLGLSTVTLGHCVDTPYPSNDRCHCPCPGNGMVSRCRSQ 60

Qy 61 NTVCRCPCGGFNDVYSSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQPLDSYK 120
Db 61 NTVCRCPCGGFNDVYSSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQPLDSYK 120

Qy 121 PGVDCAPCPGPHSPGDNOACKPWTCTAGKHTTLPASNSSDAICEDRDPPTQOETQ 180
Db 121 PGVDCAPCPGPHSPGDNOACKPWTCTAGKHTTLPASNSSDAICEDRDPPTQOETQ 180

Qy 181 GPAPRITVQPTWAMPRTSGSPSTRVEVPGRAVAAILGLVLGLPLAILLALYL 240
Db 181 GPAPRITVQPTWAMPRTSGSPSTRVEVPGRAVAAILGLVLGLPLAILLALYL 240

Qy 241 RRDORLPDAHKPPGGGSRFTPIQEOADAHSTLAKI 277
Db 241 RRDORLPDAHKPPGGGSRFTPIQEOADAHSTLAKI 277

RESULT 2
US-08-195-967-2
; Sequence 2, Application US/08195967
; Patent No. 6242566
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-195-967-2

Query Match 100.0%; Score 277; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1,4e-260; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCVGARRLGRPCALLLLGLSTVTLGHCVDTPYPSNDRCHCPCPGNGMVSRCRSQ 60
Db 1 MCVGARRLGRPCALLLLGLSTVTLGHCVDTPYPSNDRCHCPCPGNGMVSRCRSQ 60

Qy 61 NTVCRCPCGGFNDVYSSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQPLDSYK 120
Db 61 NTVCRCPCGGFNDVYSSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQPLDSYK 120

Qy 121 PGVDCAPCPGPHSPGDNOACKPWTCTAGKHTTLPASNSSDAICEDRDPPTQOETQ 180
Db 121 PGVDCAPCPGPHSPGDNOACKPWTCTAGKHTTLPASNSSDAICEDRDPPTQOETQ 180

Qy 181 GPAPRITVQPTWAMPRTSGSPSTRVEVPGRAVAAILGLVLGLPLAILLALYL 240
Db 181 GPAPRITVQPTWAMPRTSGSPSTRVEVPGRAVAAILGLVLGLPLAILLALYL 240

Qy 241 RRDORLPDAHKPPGGGSRFTPIQEOADAHSTLAKI 277
Db 241 RRDORLPDAHKPPGGGSRFTPIQEOADAHSTLAKI 277

RESULT 3
US-09-006-353A-12
; Sequence 12, Application US/09006353A
; Patent No. 6261801
; GENERAL INFORMATION:
; APPLICANT: WEI, YING-FEI
; APPLICANT: YU, GUO-LIANG
; APPLICANT: GENTZ, REINER
; APPLICANT: RUBEN, STEVEN
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/006,353A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF341
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-006-353A-12

Query Match 100.0%; Score 277; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1,4e-260; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCVGARRLGRPCALLLLGLSTVTLGHCVDTPYPSNDRCHCPCPGNGMVSRCRSQ 60
Db 1 MCVGARRLGRPCALLLLGLSTVTLGHCVDTPYPSNDRCHCPCPGNGMVSRCRSQ 60

Qy 61 NTVCRCPCGGFNDVYSSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQPLDSYK 120
Db 61 NTVCRCPCGGFNDVYSSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQPLDSYK 120

Qy 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQAPSNSSDAICEDRDPATOPQETQ 180
Db 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQAPSNSSDAICEDRDPATOPQETQ 180
Qy 181 GPPARPITVQTEAMPRTSOGSPSTRPVPGRAVAAILGLVGLGPIALILATLYL 240
Db 181 GPPARPITVQTEAMPRTSOGSPSTRPVPGRAVAAILGLVGLGPIALILATLYL 240
Qy 241 RRDRLPDDAHKPPGGGSRFTPIQEOQADAHSTLAKI 277
Db 241 RRDRLPDDAHKPPGGGSRFTPIQEOQADAHSTLAKI 277

RESULT 4

US-08-472-940-2
; Sequence 2, Application US/08472940
; Patent No. 6277962
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Buck, David
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Khourie and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/472,940
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/147,784
; FILING DATE: 03-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 277 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-472-940-2

Query Match 100.0%; Score 277; DB 4; Length 277;
Best Local Similarity 100.0%; Pred. No. 1.4e-260;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCVGARRIRGRPCALLLLGLSTVYTGHCYGDYPPSNDRCCHCRGNGVSRCSRSQ 60
Db 1 MCVGARRIRGRPCALLLLGLSTVYTGHCYGDYPPSNDRCCHCRGNGVSRCSRSQ 60
Qy 61 NTVCAPCGPGFYNDVSSPKCKPCTWCNLRSGSERKQICTATQDVTVCRCRACGTQPLDSYK 120
Db 61 NTVCAPCGPGFYNDVSSPKCKPCTWCNLRSGSERKQICTATQDVTVCRCRACGTQPLDSYK 120
Qy 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQAPSNSSDAICEDRDPATOPQETQ 180
Db 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQAPSNSSDAICEDRDPATOPQETQ 180

Db 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQAPSNSSDAICEDRDPATOPQETQ 180
Qy 181 GPPARPITVQTEAMPRTSOGSPSTRPVPGRAVAAILGLVGLGPIALILATLYL 240
Db 181 GPPARPITVQTEAMPRTSOGSPSTRPVPGRAVAAILGLVGLGPIALILATLYL 240
Qy 241 RRDRLPDDAHKPPGGGSRFTPIQEOQADAHSTLAKI 277
Db 241 RRDRLPDDAHKPPGGGSRFTPIQEOQADAHSTLAKI 277

RESULT 5

US-08-866-545-10
; Sequence 10, Application US/08866545
; Patent No. 6265535
; GENERAL INFORMATION:
; APPLICANT: Greene, Mark I.
; APPLICANT: Murali, Ramachandran
; APPLICANT: Takasaki, Wataru
; TITLE OF INVENTION: PEPTIDES AND PEPTIDE
; TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2811
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/866,545
; FILING DATE: 30-MAY-1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-493-4935
; TELEFAX: 650-493-5556
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 56 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 6265535e
; US-08-866-545-10

Query Match 20.2%; Score 56; DB 4; Length 56;
Best Local Similarity 100.0%; Pred. No. 4.1e-47;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 CRPCGGPGFYNDVSSPKCKPCTWCNLRSGSERKQICTATQDVTVCRCRACGTQPLDSY 119
Db 64 CRPCGGPGFYNDVSSPKCKPCTWCNLRSGSERKQICTATQDVTVCRCRACGTQPLDSY 119

RESULT 6

US-08-050-319B-44
; Sequence 44, Application US/08050319B

```
Patent No. 5633145
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
NUMBER OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robblins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319B
FILING DATE: 10-May-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Robblins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-050-319B-44

Query Match      4.3%; Score 12; DB 1; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149
Db 12 NOACKPWTNCTL 23

RESULT 7
US-08-465-982-44
Sequence 44, Application US/08465982
Patent No. 5863786
GENERAL INFORMATION:
APPLICANT: M.Feldmann, P.W. Gray,
APPLICANT: M.J.C. Turner, F.M Brennan
TITLE OF INVENTION: Modified human TNFalpha (Tumor
NUMBER OF INVENTION: Necrosis Factor alpha) Receptor
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Reed & Robblins
STREET: 635 Bryant Street
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,982
```

```
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/050,319
FILING DATE: 10-May-1993
ATTORNEY/AGENT INFORMATION:
NAME: Robblins, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 5150-0030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-465-982-44

Query Match      4.3%; Score 12; DB 2; Length 41;
Best Local Similarity 100.0%; Pred. No. 0.00013;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149
Db 12 NOACKPWTNCTL 23

RESULT 8
US-08-468-560C-8
Sequence 8, Application US/08468560C
Patent No. 6270998
GENERAL INFORMATION:
APPLICANT: NAGATA, Shigekazu
APPLICANT: ITOH, Naoto
APPLICANT: YONEHARA, Shin
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE
NUMBER OF INVENTION: ANTIGEN
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.
STREET: P.O. BOX 747
CITY: FALLS CHURCH
STATE: VA
COUNTRY: USA
ZIP: 22040-0747
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,560C
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR., GERLAD M.
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 20-4393P
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEFAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-468-560C-8
```

Query Match 4.3%; Score 12; DB 4; Length 133;
Best Local Similarity 100.0%; Pred. No. 0.00039;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
Db 104 NOACKPWTNCTL 115

RESULT 9
US-08-219-237B-8
; Sequence 8, Application US/08219237B
; Patent No. 5874546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Hellwege
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: James W. Hellwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 139 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-219-237B-8

Query Match 4.3%; Score 12; DB 2; Length 139;
Best Local Similarity 100.0%; Pred. No. 0.0004;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
Db 110 NOACKPWTNCTL 121

RESULT 10
US-08-477-347-17
; Sequence 17, Application US/08477347
; Patent No. 6232446
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; TITLE OF INVENTION: TNF LIGANDS

NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NETMARK
STREET: 419 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,347
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/115,685
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 106271
; FILING DATE: 08-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Townsend, G. Kevin
; REGISTRATION NUMBER: 34,033
; REFERENCE/DOCKET NUMBER: WALLACH=10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-477-347-17

Query Match 4.3%; Score 12; DB 4; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
Db 111 NOACKPWTNCTL 122

RESULT 11
US-08-476-862-8
; Sequence 8, Application US/08476862
; Patent No. 6262239
; GENERAL INFORMATION:
; APPLICANT: WALLACH, David
; APPLICANT: BIGDA, Jacek
; APPLICANT: BELETSKY, Igor
; APPLICANT: METT, Igor
; APPLICANT: ENGELMANN, Hartmut
; TITLE OF INVENTION: TNF INHIBITORS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NETMARK
; STREET: 419 Seventh Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

```

; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,862
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: IL 107267
; FILING DATE: 12-OCT-1993
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: IL 94039
; FILING DATE: 06-APR-1990
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: IL 91229
; FILING DATE: 06-AUG-1989
; PRIORITY INFORMATION DATA:
; APPLICATION NUMBER: IL 90339
; FILING DATE: 18-MAY-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, ROGER L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH-12A
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 140 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-476-862-8

Query Match      4.3%; Score 12; DB 4; Length 140;
Best Local Similarity 100.0%; Pred. No. 0.00041;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149
DB 111 NOACKPWTNCTL 122

RESULT 12
US-08-974-022-51
; Sequence 51, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-51
```

```

Query Match      4.3%; Score 12; DB 3; Length 205;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 138 NOACKPWTNCTL 149
DB 135 NOACKPWTNCTL 146
```

```

RESULT 13
US-08-795-445A-51
; Sequence 51, Application US/08795445A
; Patent No. 6284485
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavenland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 205 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-445A-51
```

```

Query Match      4.3%; Score 12; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 138 NOACKPWTNCTL 149
DB 135 NOACKPWTNCTL 146
```

RESULT 14
US-08-795-447A-51
Sequence 51, Application US/08795447A
Patent No. 6284728
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: Osteoprotegerin
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: One Amgen Center Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91362-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,447A
FILING DATE:
CLASSIFICATION: 51A
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378D2
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-447A-51

Query Match 4.3%; Score 12; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
DB 135 NOACKPWTNCTL 146

RESULT 15
US-08-974-186-51
Sequence 51, Application US/08974186
Patent No. 6284740
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-186-51

Query Match 4.3%; Score 12; DB 4; Length 205;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
DB 135 NOACKPWTNCTL 146

RESULT 16
US-08-795-446B-51
Sequence 51, Application US/08795446B
Patent No. 6288032
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavilland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,446B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-446B-51

Query Match 4.3%; Score 12; DB 4; Length 205;

Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 NOACKPWTNCTL 149
DB 135 NOACKPWTNCTL 146

RESULT 17

US-08-097-827-7
Sequence 7, Application US/08097827

GENERAL INFORMATION:

APPLICANT: Baum, Peter

Goodwin, Ray

Fanslow, William

Gayle, Richard

TITLE OF INVENTION: Novel cytokine which is a ligand for

OX40

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/097,827

FILING DATE: 23-Jul-1993

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2806

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0730

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 206 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-08-097-827-7

Query Match 4.3%; Score 12; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149

DB 136 NOACKPWTNCTL 147

RESULT 18

US-08-494-574-7

Sequence 7, Application US/08494574

Patent No. 5783665

GENERAL INFORMATION:

APPLICANT: Baum, Peter

Goodwin, Ray

Fanslow, William

Gayle, Richard

TITLE OF INVENTION: No. 5783665el cytokine which is a ligand for

OX40

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/494,574

FILING DATE: 22-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/097,827

FILING DATE: 23-JUL-1993

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2806

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0730

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 206 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-494-574-7

Query Match 4.3%; Score 12; DB 1; Length 206;
Best Local Similarity 100.0%; Pred. No. 0.00058;
Matches 12: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149

DB 136 NOACKPWTNCTL 147

RESULT 19

US-08-097-827-11

Sequence 11, Application US/08097827

GENERAL INFORMATION:

APPLICANT: Baum, Peter

Goodwin, Ray

Fanslow, William

Gayle, Richard

TITLE OF INVENTION: Novel cytokine which is a ligand for

OX40

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/097,827

FILING DATE: 23-Jul-1993

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2806

TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-08-097-827-11

Query Match 4.3%; Score 12; DB 1; Length 438;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
Db 136 NOACKPWTNCTL 147

RESULT 20
US-08-494-574-11
; Sequence 11, Application US/08494574
; Patent No. 5783665
; GENERAL INFORMATION:
; APPLICANT: Baum, Peter
; APPLICANT: Goodwin, Ray
; APPLICANT: Fanslow, William
; APPLICANT: Gayle, Richard
; TITLE OF INVENTION: No. 5783656el Cytokine which is a ligand for
; TITLE OF INVENTION: 0X40
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/494,574
; FILING DATE: 22-JUN-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/097,827
; FILING DATE: 23-JUL-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia A.
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2806
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-587-0730
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 438 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-494-574-11

Query Match 4.3%; Score 12; DB 1; Length 438;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
Db 136 NOACKPWTNCTL 147

Db 136 NOACKPWTNCTL 147

RESULT 21
US-08-996-139-15
; Sequence 15, Application US/08996139
; Patent No. 6017729
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation, Law Department
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Apple Power Macintosh
; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/996,139
; FILING DATE: 22 DECEMBER 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 60/064,671
; FILING DATE: 14 OCTOBER 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/813,509
; FILING DATE: 07 MARCH 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: USSN 08/772,330
; FILING DATE: 23 DECEMBER 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Perkins, Patricia Anne
; REGISTRATION NUMBER: 34,693
; REFERENCE/DOCKET NUMBER: 2851-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)587-0430
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 625 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-996-139-15

Query Match 3.2%; Score 9; DB 3; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149
Db 170 CKPWTNCTL 178

RESULT 22
US-08-995-659-15
; Sequence 15, Application US/08995659
; Patent No. 6242213
; GENERAL INFORMATION:
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Galibert, Laurent
; APPLICANT: Maraskovsky, Eugene
; TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB
; NUMBER OF SEQUENCES: 19

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Immunex Corporation, Law Department
;; STREET: 51 University Street
;; CITY: Seattle
;; STATE: WA
;; COUNTRY: USA
;; ZIP: 98101
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: floppy disk
;; COMPUTER: Apple Power Macintosh
;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/995,659
;; FILING DATE: 22 DECEMBER 1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 60/064,671
;; FILING DATE: 14 OCTOBER 1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;;
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2852-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;; TELEFAX: (206)233-0644
;;
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 625 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-995-659-15

Query Match 3.2%; Score 9; DB 4; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149
DB 170 CKPWTNCTL 178

RESULT 23
US-09-215-649A-15
Sequence 15 Application US/09215649A
Patent No. 6271349
GENERAL INFORMATION:
APPLICANT: Anderson, Dirk M.
Galibert, Laurent
Maraskovsky, Eugene
TITLE OF INVENTION: Receptor Activator of NF-kappaB
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation, Law Department
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: Apple Power Macintosh

;; OPERATING SYSTEM: Apple Operating System 7.5.5
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/215,649A
;; FILING DATE: 17-Dec-1998
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/996,139
;; FILING DATE: <Unknown>
;; APPLICATION NUMBER: USSN 08/813,509
;; FILING DATE: 07 MARCH 1997
;; APPLICATION NUMBER: USSN 08/772,330
;; FILING DATE: 23 DECEMBER 1996
;;
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Perkins, Patricia Anne
;; REGISTRATION NUMBER: 34,693
;; REFERENCE/DOCKET NUMBER: 2851-A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (206)587-0430
;;
;; INFORMATION FOR SEQ ID NO: 15:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 625 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-215-649A-15

Query Match 3.2%; Score 9; DB 4; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149
DB 170 CKPWTNCTL 178

RESULT 24
US-09-105-390-20
Sequence 20 Application US/09105390
Patent No. 6288303
GENERAL INFORMATION:
APPLICANT: Rodriguez, Raymond
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Denlinger & Associates
STREET: 350 Cambridge Ave., Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/105,390
FILING DATE: Filed herewith
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/050,675
FILING DATE: 25-JUN-97
ATTORNEY/AGENT INFORMATION:
NAME: Pelithory, Joanne R.
REGISTRATION NUMBER: P42,995
REFERENCE/DOCKET NUMBER: 2000-0455.30
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-324-0880

TELEFAX: 650-324-0960
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-105-390-20

Query Match 2.5%; Score 7; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 6.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20
Db 13 AALLLLG 19

RESULT 25
US-09-124-671-17
Sequence 17, Application US/09124671A
Patent No. 6160088
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
LENGTH: 105
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chimeric mouse TSP3-KDEL
US-09-124-671-17

Query Match 2.5%; Score 7; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20
Db 9 AALLLLG 15

RESULT 26
US-09-124-671-19
Sequence 19, Application US/09124671A
Patent No. 6160088
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: chimeric mouse TSP3-KDEL
US-09-124-671-19

Query Match 2.5%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20
Db 9 AALLLLG 15

RESULT 27
US-09-124-671-21
Sequence 21, Application US/09124671A
Patent No. 6160088
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21
LENGTH: 109
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chimeric Xenopus laevis TSP4-KDEL
US-09-124-671-21

Query Match 2.5%; Score 7; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20
Db 9 AALLLLG 15

RESULT 28
US-09-124-671-13
Sequence 13, Application US/09124671A
Patent No. 6160088
GENERAL INFORMATION:
APPLICANT: Rothman, James
APPLICANT: Mayhew, Mark
APPLICANT: Hoe, Mee
TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
FILE REFERENCE: 31488
CURRENT APPLICATION NUMBER: US/09/124,671A
CURRENT FILING DATE: 1998-07-29
NUMBER OF SEQ ID NOS: 42
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 13
LENGTH: 115
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chimeric rat comp
US-09-124-671-13

Query Match 2.5%; Score 7; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20

Db 9 AALLLG 15

RESULT 29

US-09-124-671-15
; Sequence 15, Application US/09124671A
; Patent No. 6160088
; GENERAL INFORMATION:
; APPLICANT: Rothman, James
; APPLICANT: Mayhew, Mark
; APPLICANT: Hoe, Mee
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS
; FILE REFERENCE: 3148
; CURRENT APPLICATION NUMBER: US/09/124,671A
; CURRENT FILING DATE: 1998-07-29
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 15
; LENGTH: 115
; TYPE: PRP
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chimeric rat COMP-KDEL
US-09-124-671-15

Query Match 2.5%; Score 7; DB 4; Length 115;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLG 20
Db 9 AALLLG 15

RESULT 30
US-08-478-039-110
; Sequence 110, Application US/08478039
; Patent No. 5681722
; GENERAL INFORMATION:
; APPLICANT: Newman, Roland A.
; APPLICANT: Hanna, Nabil
; APPLICANT: Raab, Ronald W.
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy
; NUMBER OF SEQUENCES: 114
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince St.
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22113-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,039
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/379,072
; FILING DATE: 25-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/912,292
; FILING DATE: 10-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/856,281
; FILING DATE: 23-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/735,064

; FILING DATE: 25-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin Esq., Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-160
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 110:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 128 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-478-039-110

Query Match 2.5%; Score 7; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AALLGL 21
Db 4 AALLGL 10

Search completed: June 18, 2002, 14:28:49
Job time: 207 sec

THIS PAGE BLANK (USPTO)

W09512673-A.

XX 11-MAY-1995.
PD 03-NOV-1994; 94MO-GB02415.
XX 03-NOV-1994; 94MO-GB02415.
PF 03-NOV-1994; 93US-0147784.
XX 03-NOV-1994; 93US-0147784.
PR (BECTON DICKINSON CO.
XX (STRD) UNIV LELAND STANFORD JUNIOR.
PA
XX Buck DW, Engleman EG, Godfrey W;
PI
XX WPI: 1995-185777/24.
DR N-PSDB; AAQ88758.
XX
XX Isolated ACT-4 receptor from activated T-cells - also its ligands and
PT antibodies, useful for treating diseases of the immune system
XX
XX Claim 1; Fig. 5; 82pp; English.
PS
XX This sequence encodes the full-length cell surface receptor ACT-4
CC isolated from activated CD4+ T-lymphocytes. The sequence may be
CC expressed in e.g. COS-7 cells. The encoded protein, its ligands or
CC fragments, and antibodies may be used for the treatment of transplant
CC rejection, graft-versus-host disease, autoimmune disease, etc.
XX
SQ Sequence 277 AA;

Query Match 100.0%; Score 277; DB 16; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.7e-250;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCVGARRLGRGPCAALLLLGLSTVYGLHCYVDITYPSNDRCHCECRPGNGMVSRSRQ 60
DB 1 mcvgarrrlgrgpcaalllllglstvtglhcyvgditypsndrchcecrpgngmvsrsrsq 60
OY 61 NNYCRPGCGFYNDVYSSKPKCKPCTWCNLRSGSERKOLCTATODTYCRCAAGTQPLDSYK 120
DB 61 nnycrpgcgfyndvyskpkckpctwcnlrsgerkqlctatdtycrcaagtcpldsyk 120
OY 121 PGVDCAPCPGHPSPGDNACRPMTNCTLAGKHTLQPASNSSAICEDRPPATPOETQ 180
DB 121 pyvdcapcpghpspgdnackpwtncitlagkhtlqpasnsdaicedrppatpgetq 180
OY 181 GPPARPITVQPTAMPRTSGPSTRPEVPGGRAVAAILGLGLVILGLPLAILLALYLL 240
DB 181 gpparpltvqpteamprtsqgstprvevpggravaaillglglvllglplailall 240
OY 241 RRDQRLPPDAHKRPGGSGFRPTIQEODAHSTLAKI 277
DB 241 rrdqrlppdahkppgsgsfrptiqeodahstlaki 277
RESULT 2
AAR79904
ID AAR79904 standard; Protein: 277 AA.
XX
AC AAR79904;
XX
DT 05-MAR-1996 (first entry)
XX
XX ACT-4-h-1 receptor sequence.
DE
XX
XX ACT-4; specific binding partner: sbd; B cells; lymphocyte; GVHD;
KW graft versus host disease; immune response; transplantation;
KW autoimmune disease; inflammation; HIV; human immunodeficiency virus;
KW HTLV; human T lymphocyte virus; inflammatory bowel disease;
KW screening; identification.
XX
OS Homo sapiens.
XX
FH Key 4 Location/Qualifiers

FT Cleavage-site 22..23 /note= "Possible cleavage site."
FT Cleavage-site 24..25 /note= "Possible cleavage site."
FT Modified-site 136..138 /label= Glycosylation site.
FT Modified-site 150..152 /label= Glycosylation site.
FT Domain 204..230 /label= Transmembrane domain.
XX
XX WO9521915-A1.
XX
XX 17-AUG-1995.
XX
XX 06-FEB-1995; 95MO-GB00238.
XX
XX 10-FEB-1994; 94US-0195967.
XX
XX (GREA/) GREAVES C P.
XX (STRD) UNIV LELAND STANFORD JUNIOR.
XX
XX Engleman EG, Godfrey W;
XX
XX WPI: 1995-293117/38.
XX N-PSDB; AAT04048.
XX
XX Ligand, ACT-4-1, to receptor on activated CD4 positive cells
XX useful in treatment of various immune diseases and conditions
XX
XX Disclosure; Figure 5; 124pp; English.
XX

CC ACT-4-1-h-1 is a specific binding partner (sbd) to the ACT-4
CC receptor polypeptide (encoded by this sequence) on the surface of
CC activated CD4 positive B cells. The sbp and its fragments are useful
CC in pharmaceutical compositions to modify a patient's immune response
CC as well as having application in the treatment of transplant
CC rejection, graft versus host disease, autoimmune disease, HIV,
CC inflammation, infectious agents, HTLV infected cells or HIV.
CC Specifically the sbd can be used to treat inflammatory bowel
CC disease. The sbd can also be used for screening for immunomodulatory
CC agents able to recognise ACT-4 and for monitoring activated CD4
CC positive cells or inhibiting infection of CD4 positive cells.
XX
SQ Sequence 277 AA;

Query Match 100.0%; Score 277; DB 16; Length 277;
Best Local Similarity 100.0%; Pred. No. 2.7e-250;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCVGARRLGRGPCAALLLLGLSTVYGLHCYVDITYPSNDRCHCECRPGNGMVSRSRQ 60
DB 1 mcvgarrrlgrgpcaalllllglstvtglhcyvgditypsndrchcecrpgngmvsrsrsq 60
OY 61 NNYCRPGCGFYNDVYSSKPKCKPCTWCNLRSGSERKOLCTATODTYCRCAAGTQPLDSYK 120
DB 61 nnycrpgcgfyndvyskpkckpctwcnlrsgerkqlctatdtycrcaagtcpldsyk 120
OY 121 PGVDCAPCPGHPSPGDNACRPMTNCTLAGKHTLQPASNSSAICEDRPPATPOETQ 180
DB 121 pyvdcapcpghpspgdnackpwtncitlagkhtlqpasnsdaicedrppatpgetq 180
OY 181 GPPARPITVQPTAMPRTSGPSTRPEVPGGRAVAAILGLGLVILGLPLAILLALYLL 240
DB 181 gpparpltvqpteamprtsqgstprvevpggravaaillglglvllglplailall 240
OY 241 RRDQRLPPDAHKRPGGSGFRPTIQEODAHSTLAKI 277
DB 241 rrdqrlppdahkppgsgsfrptiqeodahstlaki 277

RESULT 3

AAB35329
ID AAB35329 standard; Protein: 277 AA.
XX
AC AAB35329;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human OX40 protein SEQ ID NO: 3.
XX
KW Human; tumour necrosis factor receptor; TR13; TR14; infection;
KM cancer; autoimmune disease; allergy; inflammatory disease;
KW graft rejection; apoptosis; cardiovascular disease; aneurysm.
XX
OS Homo sapiens.
XX
PN WO200105834-A1.
XX
PD 25-JAN-2001.
XX
PE 14-JUL-2000; 2000WO-US19343.
XX
PR 16-JUL-1999; 99US-0144087.
PR 18-AUG-1999; 99US-0149450.
PR 20-AUG-1999; 99US-0149712.
PR 10-SEP-1999; 99US-0153089.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Ni J, Young PE.
XX
DR WPI: 2001-112682/12.
XX
PT Nucleic acids encoding 2 human tumor necrosis factor receptor
PT polypeptides (TR13) and (TR14); useful for the prevention, diagnosis
PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and
PT hypohidrotic ectodermal dysplasia -
XX
PS Disclosure; Page 372-373; 418pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human tumour necrosis factor receptors TR13 and TR14. These sequences are
CC useful in the diagnosis and treatment of many diseases, including cancer,
CC autoimmune diseases, cardiovascular disorders, allergies,
CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and
CC infections.
XX
SQ Sequence 277 AA;

Query Match 100.0%; Score 277; DB 22; Length 277;
Best Local Similarity 100.0%; Pred. No. 2,7e-250;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
AAB50522
ID AAB50522 standard; Protein: 277 AA.
XX
AC AAB50522;
XX
DT 15-MAR-2001 (first entry)
XX
DE Human tumour necrosis factor receptor OX40 protein SEQ ID NO:12.
XX
KW Human; tumour necrosis factor receptor 5; TR1D; TNFR-5; TR5; neutrotic;
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;
KW apoptotic cell death related disease; autoimmune disorder;
KW cardiovascular disorder; viral infection.
XX
OS Homo sapiens.
XX
PN WO200071150-A1.
XX
PD 30-NOV-2000.
XX
PE 18-MAY-2000; 2000WO-US13515.
XX
PR 20-MAY-1999; 99US-0135164.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Wel Y, Ruben SM, Gentz RU, Ni J;
XX
DR WPI: 2001-041051/05.
XX
PT Nucleic acid encoding a TR1D polypeptide, also referred to as tumor
PT necrosis factor receptor 5, useful in the diagnosis, treatment or
PT prevention of cancer, autoimmune disorders and viral infection -
XX
PS Disclosure; Fig 2; 285pp; English.
XX
CC The present invention describes the human TR1D protein (tumour necrosis
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without
CC intracellular domain, also referred to as tumour necrosis factor
CC receptor 5 (TNFR-5 or TR5)). TR1D has cytostatic, immunosuppressive,
CC neutrotic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic
CC activities, and can be used in gene therapy. The TR1D polynucleotides
CC are useful for detecting complementary polynucleotides. TR1D proteins and
CC polynucleotides are useful in the treatment of tumours, resistance to
CC parasite, bacteria and viruses, restenosis and graft versus host disease.
CC They are also useful for inducing proliferation of T-cells, endothelial
CC cells and certain haematopoietic cells, to regulate antiviral responses
CC and to prevent certain autoimmune diseases after stimulation of TR1D by
CC an agonist or TRAIL binding facilitator. The antibodies which bind TR1D
CC polypeptides are useful for treating and/or preventing diseases
CC associated with increased or decreased apoptotic cell death. The TR1D
CC polynucleotides, proteins, antibodies, agonists and antagonists are
CC useful in the diagnosis, treatment or prevention of: (a) cancer;
CC (b) autoimmune disorders; (c) diseases associated with increased
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The
CC present sequence represents a tumour necrosis factor receptor used in
CC comparison with TR1D in the exemplification of the present invention.
XX
SQ Sequence 277 AA;

Query Match 100.0%; Score 277; DB 22; Length 277;
Best Local Similarity 100.0%; Pred. No. 2,7e-250;
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVGARRLGRPCAAALLLGLSTVTVGLHCVGDTYPSNDRCHBRCRPGNGVNSRCSRSQ 60

```

Db      1  |mcvgarrligrpcaalllllgistvtglhcvygdtypsndrcchecrpngmvsrscsq 60
Oy      61  |NTVCRPCGPGFYNDVVSRSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQ 120
Db      61  |ntvcrrpcpgfyndvvsrskpckpctwcnlrsgerkqlctacqdlvrcrcragtq 120
Oy     121  |PCVDCAPCPGPHFSPGDNOACKRWNTCLAGKHTLQPASNSDALCEDRDPATOPQETQ 180
Db     121  |pvcdcapcpghfispgdngackpwtncclagkhtlqpasnsdalcedrdpatqg 180
Oy     181  |GPARPRITVQPTFAMPRTSQSGSTRVREVGGRVAVALLGLGLVGLLPLALLLYLL 240
Db     181  |gpaprprltvqprtsqsgstrvrevggrvavallglglvlgllplallllyll 240
Oy     241  |RRDQRLPPDAHKPCGGSFRTPIQEQADAHSTIAKI 277
Db     241  |rrdqrlppdahkpcggfstrtpiqeqadahanstlaki 277

RESULT   5
AAR76996
ID      AAR76996 standard; Protein; 277 AA.
XX
AC      AAR76996;
XX
DT      21-DEC-1995 (first entry)
XX
DE      Deduced sequence encoded by human OX-40 cDNA.
XX
KW      Human OX-40; activated T-cells; CD4+ T-cells; antigen;
KW      multiple sclerosis; sarcoidosis; rheumatoid arthritis; uveitis;
KW      T-cell lymphoma.
XX
OS      Homo sapiens.
XX
PN      WO9521251-A.
XX
PD      10-AUG-1995.
XX
PE      06-FEB-1995; 95WO-CB00237.
XX
PR      04-FEB-1994; 94US-0192480.
XX
PA      (WEIN/) WEINBERG A D.
PA      (CANT-) CANTAB PHARM RES LTD.
XX
PI      Vandenberg AA, Weinberg AD;
XX
DR      WPI: 1995-283771/37.
DR      N-PSDB: AAO93257.
XX
PT      Nucleic acid encoding an activated T-cell antigen, OX-40 - used to
PT      develop prods. for detection and therapy of conditions mediated by
PT      activated T-cells, eg. multiple sclerosis, rheumatoid arthritis, etc.
XX
PS      Claim 3; Fig 11; 91pp; English.
XX
CC      Antigen OX-40 is specifically expressed on the cell surface of
CC      antigen activated T-cells, especially, for example, CD4+ T-cells. A
CC      human cDNA encoding the human OX-40 homologue was cloned as follows.
CC      Using the Experimental Autoimmune Encephalomyelitis model in rats
CC      the OX-40 antigen was identified (expressed on the surface of
CC      activated autanigen-specific CD4+ T-cells present at the site of
CC      inflammation but absent on CD4+ T-cells at non-inflammatory sites)
CC      and cDNA encoding the antigen was isolated. PCR primers were
CC      designed and used to clone murine OX-40 cDNA by PCR from RNA
CC      isolated from murine CD4+ T-cells activated with concanavalin A.
CC      Then the murine OX-40 cDNA was used to probe a cDNA lambda gt11
CC      library from human activated T lymphocytes to obtain human OX-40
CC      cDNA. The published patent application states that the OX-40 cDNA
CC      sequence is also in SO ID no. 1, but this sequence is not present
CC      in the spec. A nucleic acid having the sequence in SO ID no 1 and

```

```

CC      the polypeptide encoded by it are claimed.
XX
SO      Sequence      277 AA:

Query Match      41.2%; Score 114; DB 16; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  |mcvgarrligrpcaalllllgistvtglhcvygdtypsndrcchecrpngmvsrscsq 60
Db      1  |mcvgarrligrpcaalllllgistvtglhcvygdtypsndrcchecrpngmvsrscsq 60
Oy     61  |NTVCRPCGPGFYNDVVSRSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQ 114
Db     61  |ntvcrrpcpgfyndvvsrskpckpctwcnlrsgerkqlctacqdlvrcrcragtq 114

RESULT   6
AAM94649
ID      AAM94649 standard; peptide; 56 AA.
XX
AC      AAM94649;
XX
DT      29-APR-1999 (first entry)
XX
DE      TNF-R extracellular Cys-rich domain OX40.
XX
KW      Tumour necrosis factor receptor; TNF-R; autoimmune diseases;
KW      inflammation; septic shock; cachexia; graft versus host disease;
KW      skin allergic reaction; immune complex disease; malaria;
KW      transplantation rejection.
XX
OS      Homo sapiens.
XX
PN      WO9853842-A1.
XX
PD      03-DEC-1998.
XX
PE      29-MAY-1998; 98WO-US10891.
XX
PR      30-MAY-1997; 97US-0866545.
XX
PA      (UYPE-) UNITV PENNSYLVANIA.
XX
PI      Greene MI, Murali R, Takasaki W;
XX
DR      WPI: 1999-080781/07.
XX
PT      New compounds designed from a binding loop of a tumour necrosis
PT      factor receptor - are capable of inhibiting the biological
PT      activities of tumour necrosis factor, e.g., in treating inflammation
PT      or autoimmune diseases
XX
PS      Disclosure; Fig 1: 78pp; English.
XX
CC      The present invention describes peptides and peptide analogues which
CC      correspond in primary sequence to a binding loop of a tumour necrosis
CC      factor receptor (TNF-R) superfamily member. The compounds are especially
CC      designed from a binding loop of TNF-R p55. They are capable of
CC      inhibiting TNF binding to its cellular receptors and may be used to
CC      inhibit the biological activities of TNF. They may be used in treating
CC      TNF-associated conditions such as acute and chronic inflammatory
CC      responses, septic shock, cachexia, autoimmunity, graft-versus-host
CC      disease, skin allergic reactions, immune complex disease,
CC      transplantation rejection and malaria. Administration is, e.g. oral,
CC      transdermal, transmucosal, pulmonary, subcutaneous, intravenous or
CC      intramuscular. Parenteral dosage is 0.1-5 mg/kg/day. The present
CC      sequence represents an extracellular Cys-rich domain of TNF-R from the
CC      present invention.
XX
SO      Sequence      56 AA:

```

Query Match 20.2%; Score 56; DB 20; Length 56;
 Best Local Similarity 100.0%; Pred. No. 1,4e-44;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 CRPCGPGFYNDVSSKPKCTWCMNLRSGSERKOLCTATODTVCRCRAGTGPLDSY 119
 Db 1 crpcpgpfyndvsskpkctwcmnlrsgerkqlctatqdtvcrcragtqpldsy 56

RESULT 7

AAB69201
 ID AAB69201 standard; protein; 58 AA.

AC AAB69201;

DE 30-APR-2001 (first entry)

XX Human TNF-R extracellular Cys-rich domain OX40 SEQ ID NO:10.

XX Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;

KW osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic;

KW antirheumatic; antiarthritic; antiinflammatory; immunomodulatory;

KW tumour necrosis factor-related activation-induced cytokine; TRANCE;

KW receptor activator of NF-kappaB ligand; RANK; osteoporosis;

KW periodontal disease; metastatic bone disease; rheumatoid arthritis;

KW T cell proliferation; CD40 receptor system.

XX Homo sapiens.

XX WO200108699-A1.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-US20510.

XX 28-JUL-1999; 99US-0146090.

XX (UYPE-) UNIV PENNSYLVANIA.

XX (AOKI/) AOKI K.

XX (HORN/) HORNE W C.

XX (BARO/) BARON R.

XX Aoki K, Horne WC, Baron R, Greene MI, Murali R;

XX WPT: 2001-182866/18.

XX Use of peptides and peptide analogs which are TRANCE/RANK inhibitors,

XX for inhibiting osteoclastogenesis and bone resorption

XX Disclosure: Fig 1; 81pp: English.

XX The present invention describes a method for inhibiting

XX osteoclastogenesis and bone resorption. Osteoclastogenesis and bone

XX resorption inhibiting peptide analogues from the present invention have

XX osteopathic, cytostatic, antirheumatic, antiarthritic, antiinflammatory

XX and immunomodulatory activities, and are tumour necrosis factor (TNF)-

XX related activation-induced cytokine (TRANCE)/receptor activator of

XX NF-kappaB ligand (RANK) inhibitors. The method is useful for treating

XX diseases characterised by bone loss such as osteoporosis, Paget's

XX disease, metastatic bone disease, rheumatoid arthritis or periodontal

XX disease, and modulating dendritic cell maturation, T cell proliferation,

XX and/or CD40 receptor systems. The present sequence represents an

XX extracellular Cys-rich domain of a tumour necrosis factor receptor

XX (TNF-R) superfamily member, which is used in the exemplification of

XX the present invention.

SO Sequence 58 AA;

Query Match 15.2%; Score 42; DB 22; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1,7e-31;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 CRPCGPGFYNDVSSKPKCTWCMNLRSGSERKOLCTATODTVCRCRAGTGPLDSY 105
 Db 1 crpcpgpfyndvsskpkctwcmnlrsgerkqlctatqdt 42

RESULT 8

AAB84272
 ID AAB84272 standard; peptide; 37 AA.

AC AAB84272;

DE 22-AUG-2001 (first entry)

XX Secondary signalling sequence used to make cytoplasmic signalling motif.

KW Stimulatory primary signalling motif; immune cell; signal transduction;

KW chimeric receptor; inflammatory disease; autoimmune disease; asthma;

KW eczema; congenital disease; cystic fibrosis; sickle cell anemia;

KW dermatological disease; psoriasis; neurological disease;

KW multiple sclerosis; transplant-related disease; metabolic disease;

KW organ transplant rejection; graft versus host disease;

KW idiopathic disease; diabetes; cancer.

XX Synthetic.

XX WO200132709-A2.

XX 10-MAY-2001.

XX 01-NOV-2000; 2000WO-GB04183.

XX 01-NOV-1999; 99GB-0025848.

XX (CELL-) CELTECH CHIROSCIENCE LTD.

XX Finney HM, Lawson ADG;

XX WPT: 2001-389718/41.

XX Novel cytoplasmic signalling protein and chimeric receptor protein,

XX useful for treating HIV infection, asthma, eczema, psoriasis, multiple

XX sclerosis, contain non-natural stimulatory primary signalling motif -

XX Claim 15; Page 29; 45pp: English.

XX The present sequence represents a secondary signalling sequence, which

XX is linked to a non-natural stimulatory primary signalling motif to

XX produce a cytoplasmic signalling motif. The primary motif is efficient

XX at mediating immune cell signal transduction, particularly when

XX incorporated in an intracellular signalling domain of a chimeric

XX receptor. The primary signalling motif can be combined in any way so

XX as to achieve the desired level of activation (or inhibition) of a

XX number of secondary messenger cascades. The signalling motifs are useful

XX in therapy and in the manufacture of medicament for treating or

XX preventing disease in humans or animals. They are useful for treating

XX human patients suffering from infectious diseases e.g. human

XX immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases

XX such as asthma and eczema, congenital diseases e.g. cystic fibrosis,

XX sickle cell anemia, dermatological diseases e.g. psoriasis, neurological

XX diseases e.g. multiple sclerosis, transplant-related disease e.g. organ

XX transplant rejection, graft versus host disease, metabolic/idiopathic

XX disease e.g. diabetes, and cancer.

SO Sequence 37 AA;

Query Match 13.4%; Score 37; DB 22; Length 37;
 Best Local Similarity 100.0%; Pred. No. 5.3e-27;
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 241 RRDORLPPDAHKRPPGGSFRTPIQEOBDAHSTLAKI 277

Db 1 rrdqrlppdahkppggsftrtpeqadahnstlakt 37

RESULT 9

AAB98799 ID AAB98799 standard; Peptide: 37 AA.

AC AAB98799; .

DT 08-AUG-2001 (first entry)

DE Human secondary signalling motif SB34a.

KW Human; anti-HIV; antiinflammatory; antiaesthetic; dermatological;
KW antischlicking; antipsoriatic; neuroprotective; immunosuppressive;
KW antidiabetic; cytostatic; HIV infection; inflammation;
KW autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;
KW neurological disease; organ transplant rejection; diabetes; cancer;
KW graft-versus-host disease; adaptor receptor protein; CD28; CD134; CD154;
KW primary signalling motif; secondary signalling motif.

OS Homo sapiens.

XX WO200132866-A2.

PN 10-MAY-2001.

PD 01-NOV-2000; 2000WO-GB04189.

PF 01-NOV-1999; 99GB-0025854.

PR (CELL-) CELLTech CHIROSCIENCE LTD.

PA Flinney HM, Lawson ADG;

PI WPI: 2001-328790/34.

DR Novel polynucleotide encoding adaptor receptor protein useful for

PT treating human immunodeficiency virus (HIV) infection, asthma, cystic

PT fibrosis, multiple sclerosis, organ transplant rejection, diabetes and

PT cancer -

PS Claim 26; Page 35; 52pp; English.

XX The invention relates to a novel nucleic acid encoding an adaptor
CC receptor protein comprising an extracellular ligand-binding domain, a
CC transmembrane domain and an intracellular signalling domain. The
CC intracellular signalling domain comprises the cytoplasmic portion of at
CC least one adaptor protein, and the extracellular ligand-binding domain
CC is not CD8 or a major histocompatibility complex (MHC) class I protein.
CC The adaptor receptor protein and the nucleic acid encoding it are useful
CC in therapy. They are useful in the manufacture of a medicament for the
CC treatment or prevention of disease in humans and animals. They are useful
CC in the treatment of infectious diseases (e.g. HIV infection),
CC inflammatory and autoimmune diseases (e.g. asthma and eczema),
CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia),
CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g.)
CC multiple sclerosis), organ transplant rejection, graft-versus-host
CC disease and metabolic/idiopathic diseases such as diabetes and cancer.
CC The present sequence is a secondary signalling motif used in the
CC invention. Secondary signalling motifs impart secondary or co-stimulatory
CC signalling capacity to a molecule in T cells. They may be used as
CC components of the adaptor receptor protein of the invention. Motifs were
CC isolated from CD28, CD134 and CD154.

XX Sequence 37 AA:

Query Match 13.4%; Score 37; DB 22; Length 37;
Best Local Similarity 100.0%; Pred. No. 5.3e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 RRDQLPPDAHKKPGGSEFRTPIQEQADAHSTLAKI 277

Db 1 rrdqrlppdahkppggsftrtpeqadahnstlakt 37

RESULT 10

AAB84292 ID AAB84292 standard; peptide: 41 AA.

AC AAB84292;

DT 22-AUG-2001 (first entry)

DE Amino acid sequence of a secondary signalling sequence.

KW Stimulatory primary signalling motif; immune cell; signal transduction;
KW chimeric receptor; inflammatory disease; autoimmune disease; asthma;
KW eczema; congenital disease; cystic fibrosis; sickle cell anaemia;
KW dermatological disease; psoriasis; neurological disease;
KW multiple sclerosis; transplant-related disease; metabolic disease;
KW organ transplant rejection; graft versus host disease;
KW idiopathic disease; diabetes; cancer.

OS Synthetic.

XX WO200132709-A2.

PN 10-MAY-2001.

PD 01-NOV-2000; 2000WO-GB04183.

PF 01-NOV-1999; 99GB-0025848.

PR (CELL-) CELLTech CHIROSCIENCE LTD.

PA Flinney HM, Lawson ADG;

PI WPI: 2001-389718/41.

DR Novel cytoplasmic signalling protein and chimeric receptor protein,

PT useful for treating HIV infection, asthma, eczema, psoriasis, multiple

PT sclerosis, contain non-natural stimulatory primary signalling motif -

PS Example 2; Fig 4; 45pp; English.

XX The present sequence represents a secondary signalling sequence, which
CC may be linked to a non-natural stimulatory primary signalling motif
CC The primary motif is efficient at mediating immune cell signal
CC transduction, particularly when incorporated in an intracellular
CC signalling domain of a chimeric receptor. The primary signalling motif
CC can be combined in any way so as to achieve the desired level of
CC activation (or inhibition) of a number of secondary messenger cascades.
CC The signalling motifs are useful in therapy and in the manufacture of
CC medicament for treating or preventing disease in humans or animals. They
CC are are useful for treating human patients suffering from infectious
CC diseases e.g. human immunodeficiency virus (HIV) infections,
CC inflammatory/autoimmune diseases such as asthma and eczema, congenital
CC diseases e.g. cystic fibrosis, sickle cell anaemia, dermatological
CC diseases e.g. psoriasis, neurological diseases e.g. multiple sclerosis,
CC transplant-related disease e.g. organ transplant rejection, graft versus
CC host disease, metabolic/idiopathic disease e.g. diabetes, and cancer.

XX Sequence 41 AA:

Query Match 13.4%; Score 37; DB 22; Length 41;
Best Local Similarity 100.0%; Pred. No. 5.8e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 RRDQLPPDAHKKPGGSEFRTPIQEQADAHSTLAKI 277

Db 3 rrdqrlppdahkppggsftrtpeqadahnstlakt 39

```

13.4%; Score 37; DB 22; Length 41;
Best Local Similarity 100.0%; Pred. No. 5 Be-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

241 RRDQRLPPDAHKPPGGGSFRPTDIEEQADAHSTAKI 277
|||||

```

DB	3	rrdqrldpdahkppggsgfttrpiqeeqadahnslakl 39
RESULT	12	
ID	AAB98822	
XX	AAB98822 standard; Peptide; 41 AA.	
AC	AAB98822;	
XX		
DT	08-AUG-2001 (first entry)	
XX		
DE	Human secondary signalling motif sequence block SB34.	
XX		
KW	Human: anti-HIV; antiinflammatory; antiasthmatic; dermatological; antistickling; antiprosclerotic; neuroprotective; immunosuppressive; antidiabetic; cyostatic; HIV infection; inflammation; autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis; neurological disease; organ transplant rejection; diabetes; cancer; graft-versus-host disease; adaptor receptor protein; sequence block; SB; primary signalling motif; secondary signalling motif.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200132866-A2.	
XX		
PD	10-MAY-2001.	
XX		
PF	01-NOV-2000; 2000WO-GB04189.	
XX		
PR	01-NOV-1999; 99GB-0025854.	
XX		
PA	(CELL-) CELLTech CHIROSCIENCE LTD.	
XX		
PI	Finney HM, Lawson ADG:	
XX		
DR	WP: 2001-328790/34.	
XX		
PT	Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cystic fibrosis, multiple sclerosis, organ transplant rejection, diabetes and cancer	
XX		
PS	Example 3; Fig 4; 52pp; English.	
XX		
CC	The invention relates to a novel nucleic acid encoding an adaptor receptor protein comprising an extracellular ligand-binding domain, a transmembrane domain and an intracellular signalling domain. The intracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain is not C98 or a major histocompatibility complex (MHC) class I protein. The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the treatment or prevention of disease in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection), inflammatory and autoimmune diseases (e.g. asthma and eczema), congenital diseases (e.g. cystic fibrosis) and sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g. multiple sclerosis), organ transplant rejection, graft-versus-host disease and metabolic/diopathic diseases such as diabetes and cancer. The present sequence is one of a number of sequence blocks (SBs) of primary and secondary signalling motifs. Primary signalling motifs transduce either a stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary signalling motifs impart secondary or co-stimulatory signalling capacity to a molecule in T cells. Primary and secondary signalling motifs may be used as components of the adaptor receptor protein of the invention. The sequence contains a GS linker at the N-terminus to facilitate cloning.	
XX		
SO	Sequence 41 AA;	

Best Local Similarity 100.0%, Pred. No. 5.8e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 RRDORLPDAHKPPGGSFRTPIOEQADAHSTLAKI 277
|||||
DB 3 rrdqrlppdahkppggsftrtpiqeqadahstlakt 39

RESULT 13
AAB98752

ID AAB98752 standard; Peptide: 32 AA.

AC AAB98752;

DT 07-AUG-2001 (first entry)

DE Human secondary signalling motif SB34a.

XX Human; primary signalling motif: CD28; CD134; CD154; sequence block; SB;
KW immunosuppressive; secondary signalling sequence; antimicrobial; cancer;
KW antiinflammatory; dermatological; neuroprotective; cytostatic; anti-HIV;
KW antiaslomatic; antislaking; antipsoriatic; antidiabetic; gene therapy;
KW diabetes; immune cell signal transduction; infection; inflammation;
KW autoimmune disease; congenital disease; psoriasis; neurological disease;
KW organ transplant rejection.

XX Homo sapiens.

PN WO200132867-A1.

PD 10-MAY-2001.

PF 01-NOV-2000; 2000WO-GB04193.

PR 01-NOV-1999; 99GB-0025853.

PA (CELL-) CELLTRECH CHIROSCIENCE LTD.

PI Flinney HM, Lawson ADG;

DR WPI; 2001-328791/34.

PT New nucleic acids encoding polypeptides with expanded primary signalling
PT motifs, for use in gene therapy, particularly for treating or
PT preventing infections, inflammations or autoimmune diseases in humans

PS Claim 16; Page 28; 43pp; English.

XX The invention relates to novel primary signalling motifs containing
CC a consensus amino acid sequence. These motifs are extremely
CC efficient at mediating immune cell signal transduction, particularly
CC when incorporated into an intracellular signalling domain of a chimeric
CC receptor. Nucleic acids that encode, and polypeptides that contain,
CC these primary signalling motifs are useful in medicine and research.
CC They are useful in therapy, or in the manufacture of a medicament for
CC treating or preventing disease in humans or in animals. These diseases
CC include infections (e.g. HIV (human immunodeficiency virus) infection),
CC inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital
CC diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological
CC disorders (e.g. psoriasis), neurological diseases (e.g. multiple
CC sclerosis), organ transplant rejection or graft-versus-host disease, or
CC metabolic/adipathic diseases (e.g. diabetes or cancer). The
CC invention sequence is a secondary signalling sequence used in the
CC invention. Secondary signalling sequences impart secondary or
CC co-stimulatory signalling capacity to a molecule in T cells.
CC Secondary signalling sequences were isolated from human CD28, CD134
CC and CD154.

XX Sequence 32 AA;

Query Match: 11.6%; Score 32; DB 22; Length 32;

Best Local Similarity 100.0%, Pred. No. 2.2e-22;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 RRDORLPDAHKPPGGSFRTPIOEQADAHSTLAKI 272
|||||
DB 1 rrdqrlppdahkppggsftrtpiqeqadahstlakt 32

RESULT 14
AAB66985

ID AAB66985 standard; Protein: 205 AA.

AC AAB66985;

DT 19-APR-2001 (first entry)

DE Ox40 protein.

XX Bone loss; osteoprotegerin; OPG; rheumatoid arthritis; hyperalgesia;
KW multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;
KW systemic lupus erythematosus; graft-versus-host disease; septic shock;
KW acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain;
KW coronary condition; myocardial infarction; cancer; diabetes; psoriasis;
KW endometritis; fever; glomerulonephritis; inflammatory bowel disease;
KW ischaemia; Parkinson's disease.

XX Unidentified.

PN WO200103719-A2.

PD 18-JAN-2001.

PF 07-JUL-2000; 2000WO-US18667.

PR 09-JUL-1999; 99US-0350670.

PR 09-DEC-1999; 99US-0457647.

PA (AMGE-) AMGEN INC.

PI Boyle WJ, Lacey DL, Calzone FJ, Chang M, Senaldi G;

DR WPI; 2001-103031/11.

PT Treating conditions leading to bone loss such as rheumatoid arthritis,
PT multiple sclerosis and asthma, comprises administering an
PT osteoprotegerin protein in conjunction with e.g. inhibitors of
PT interleukin and tumor necrosis factor alpha

PS Disclosure; Fig 2; 316pp; English.

XX The present invention relates to a method for treating conditions leading
CC to bone loss. The method comprises administering a purified and isolated
CC osteoprotegerin (OPG) protein (AAE57836-AAE57838 and AAB66974-AAB66976)
CC in conjunction with other substances such as tumour necrosis factor-alpha
CC (TNF-alpha) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE
CC modulators, fibroblast growth factor (FGF)-1-10 modulators and/or platelet
CC activating factor (PAF) antagonists. The method is useful for treating
CC conditions leading to bone loss such as rheumatoid arthritis, multiple
CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also
CC useful for treating inflammation, systemic lupus erythematosus (SLE) and
CC graft-versus-host disease (GVHD). Other diseases that can be treated
CC include acute pancreatitis, Alzheimer's disease, anorexia,
CC atherosclerosis, coronary conditions (e.g. myocardial infarction),
CC cancer, diabetes, endometritis, fever, glomerulonephritis, hyperalgesia,
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,
CC psoriasis and septic shock. The present sequence was used in a sequence
CC homology comparison.

XX Sequence 205 AA;

Query Match: 4.3%; Score 12; DB 22; Length 205;
Best Local Similarity 100.0%, Pred. No. 0.0048;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
 |||||
 Db 135 nqackpwtncctl 146

RESULT 15
 AAR81881
 ID AAR81881 standard; Protein: 206 AA.

AC AAR81881;
 DT 08-JUL-1996 (first entry)
 DE Mouse type-II membrane polypeptide OX40 extracellular domain.
 XX
 KW OX40; OX40-L; cytokine; cell surface molecule;
 KM membrane glycoprotein.
 XX
 OS Mus musculus.
 XX
 PN US5457035-A.
 XX
 PD 10-OCT-1995.
 XX
 PE 23-JUL-1993; 93US-0097827.
 XX
 PR 23-JUL-1993; 93US-0097827.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
 XX
 DR WPI; 1995-357992/46.
 DR N-PSDB; AAT00826.
 XX
 PT New isolated DNA encoding the OX40 ligand polypeptide - also vectors
 PT and host cells, used to produce recombinant ligand used in e.g.
 PT prim. T cell culture, to modulate immune response etc.
 XX
 PS Example 1; Column 33-34; 26pp; English.
 XX
 CC This sequence encodes the extracellular domain of OX40, a membrane
 CC glycoprotein present on the CD4 positive subset of activated T
 CC cells.
 CC
 SQ Sequence 206 AA;

Query Match 4.3%; Score 12; DB 16; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
 |||||
 Db 136 nqackpwtncctl 147

RESULT 16
 AAW48977
 ID AAW48977 standard; Protein: 206 AA.
 XX
 AC AAW48977;
 DT 25-SEP-1998 (first entry)
 DE Mouse OX40 extracellular domain.
 XX
 KW OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L;
 KM OX40/Fc.
 XX
 OS Mus sp.

XX US5783665-A.
 PN
 XX
 PD 21-JUL-1998.
 XX
 PE 22-JUN-1995; 95US-0494574.
 XX
 PR 23-JUL-1993; 93US-0097827.
 PR 22-JUN-1995; 95US-0494574.
 XX
 PA (IMMV) IMMUNEX CORP.

PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
 XX
 DR WPI; 1998-427099/36.
 DR N-PSDB; AAV32640.
 XX
 PT Purified polypeptide OX-40 ligands - for co-stimulation of T-cell
 PT production and binding assays for OX-40 and homologues
 XX
 PS Example 1; Col 33-34; 26pp; English.
 XX
 CC The present sequence represents the mouse OX40 extracellular domain
 CC CC The extracellular domain of OX40 is its ligand binding domain. The
 CC CDNA (AAV32640) encoding OX40 extracellular domain was used in the
 CC construction of the chimeric OX40/Fc cDNA (AAV32640). The invention
 CC claims for a murine OX40-L cytokine (AAW48975) that binds to the OX40
 CC murine T cell antigen. The OX40-L protein is claimed to be useful
 CC for co-stimulation of T-cell production and in binding assays for
 CC detecting OX40 or its homologues. The OX40-L protein is also claimed
 CC to generate a TH-2 immune response.
 XX
 SQ Sequence 206 AA;

Query Match 4.3%; Score 12; DB 19; Length 206;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
 |||||
 Db 136 nqackpwtncctl 147

RESULT 17
 AAR81882
 ID AAR81882 standard; Protein: 438 AA.
 XX
 AC AAR81882;
 DT 30-MAR-1996 (first entry)
 DE Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.
 XX
 KW OX40; OX40-L; cytokine; cell surface molecule; plasmid;
 KM pDC406/OX40/Fc*; membrane glycoprotein.
 XX
 OS Synthetic.
 XX
 PN US5457035-A.
 PN
 PD 10-OCT-1995.
 PD
 PE 23-JUL-1993; 93US-0097827.
 XX
 PR 23-JUL-1993; 93US-0097827.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
 XX
 DR WPI; 1995-357992/46.
 DR N-PSDB; AAT00829.

XX New isolated DNA encoding the OX40 ligand polypeptide - also vectors
PT and host cells, used to produce recombinant ligand used in e.g.
PT prim. T cell culture, to modulate immune response etc.
XX
PS Example 2: Column 35-38; 26pp; English.
XX
CC This plasmid encodes an OX40/Fc antibody fragment mutin protein,
CC and is used to express a soluble OX40/Fc mutin fusion protein for
CC use in detecting CDNA clones encoding a OX40 ligand. The Fc
CC fragment may be derived from human IgG1, and the plasmid may be
CC used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell
CC line. Culture supernatant was purified by affinity chromatography
CC and this was used, together with labeled goat anti-human IgG to
CC screen various cell lines.
XX
SQ Sequence 438 AA:

Query Match 4.3%; Score 12; DB 16; Length 438;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 138 NOACKPWTNCTL 149
DB 136 ngackpwtncttl 147

RESULT 18
AAW48976
ID AAW48976 standard; Protein; 438 AA.
XX
AC AAW48976;
XX
DT 25-SEP-1998 (first entry)
XX
DE OX40/Fc mutin.
XX
KW OX40/Fc: cytokine; T cell antigen; TH-2 immune response; OX40-L;
KW chimeric.
XX
OS Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
FH Key Location/Qualifiers
FT Region 1..206
FT /note= "Extracellular domain of mouse OX40"
FT Region 207..438
FT /note= "Mutant Fc region of human IgG1 antibody"
FT Misc-difference 225
FT /note= "changed from Leu in wild-type to Ala in
FT mutant"
FT Misc-difference 226
FT /note= "changed from Leu in wild-type to Gly in
FT mutant"
FT Misc-difference 228
FT /note= "changed from Gly in wild-type to Ala in
FT mutant"
XX
XX US5783665-A.
XX
XX 21-JUL-1998.
XX
XX 22-JUN-1995; 95US-0494574.
XX
XX 23-JUL-1993; 93US-0097827.
XX
XX 22-JUN-1995; 95US-0494574.
XX
XX (IMMUNEX) IMMUNEX CORP.
XX
XX Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
XX
XX WPI; 1998-427099/36.
XX
XX
XX

DR N-PSDB; AAV32636.
XX
XX Purified polypeptide OX-40 ligands - for co-stimulation of T-cell
PT production and binding assays for OX-40 and homologues
XX
XX
PS Example 2: Col 37-40; 26pp; English.
XX
XX The present sequence represents the OX40/Fc fusion protein that
CC contains the extracellular domain of mouse OX40 fused to the mutated
CC Fc region of the human IgG1 antibody. The fusion protein was used
CC for detecting CDNA clones encoding an OX40 ligand. The invention
CC claims for a murine OX40-L cytokine (AAW48975) that binds to the murine
CC T cell antigen, OX40. The OX40-L protein is claimed to be useful for
CC co-stimulation of T-cell production and in binding assays for
CC detecting OX40 or its homologues. The OX40-L protein is also claimed
CC to generate a TH-2 immune response.
XX
SQ Sequence 438 AA:

Query Match 4.3%; Score 12; DB 19; Length 438;
Best Local Similarity 100.0%; Pred. No. 0.0091;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 138 NOACKPWTNCTL 149
DB 136 ngackpwtncttl 147

RESULT 19
AAV59508
ID AAV59508 standard; Protein; 201 AA.
XX
AC AAV59508;
XX
DT 31-MAR-2000 (first entry)
XX
DE OBM binding protein sequence.
XX
KW OBM-BP; OBM binding protein; osteoclast formation promoting factor;
KW bone metabolic disease; osteoporosis; therapy.
XX
OS Mus sp.
OS
XX
XX JP1332581-A.
XX
XX 07-DEC-1999.
XX
XX 20-OCT-1998; 98JP-0316973.
XX
XX 24-MAR-1998; 98JP-0076232.
XX
XX (SNOW) SNOW BRAND MILK PROD CO LTD.
XX
XX (SANY) SANKYO CO LTD.
XX
XX WPI: 2000-091362/08.
XX
XX N-PSDB; AA449022.
XX
XX A new protein, a DNA and its application
XX
XX
XX Claim 1: Page 17-18; 18pp; Japanese.
XX
XX
XX This sequence is the osteoclast formation promoting factor (OBM)
CC binding protein (OBM-BP) of the invention. The protein is useful as a
CC preventive and/or treating agent for bone metabolic diseases such as
CC osteoporosis. Substances which inhibit the binding of OBM to OBM-BP can
CC be used as biochemical reagents.
XX
XX
SQ Sequence 201 AA:

Query Match 3.2%; Score 9; DB 21; Length 201;
Best Local Similarity 100.0%; Pred. No. 3;
XX
XX
XX

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 141 CKPWTNCTL 149
 |||||
 Db 170 ckpwtnctl 178

RESULT 20
 AAM83200
 ID AAM83200 standard; Protein: 625 AA.

AC AAM83200;
 DT 11-FEB-1999 (first entry)

DE Murine osteoclast differentiation and activation receptor.

KW Osteoprotegerin binding protein; OPG binding protein; arthritis;
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODA;
 KW hypercalcaemia; osteoclast differentiation and activation receptor;
 KW Paget's disease.

OS Mus sp.

PN WO9846751-A1.

PD 22-OCT-1998.

PF 15-APR-1998; 98WO-US07584.

PR 30-MAR-1998; 98US-0052521.

PR 16-APR-1997; 97US-0842842.

PR 23-JUN-1997; 97US-0880855.

PA (AMGE-) AMGEN INC.

PI Boyle WJ;

DR WPI: 1998-594578/50.

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,
 PT e.g. treating bone diseases by modulating osteoclast differentiation
 PT and for diagnosis

PS Example 12; Fig 10; 47pp; English.

XX The present sequence represents murine osteoclast differentiation
 CC and activation receptor (ODAR). The present invention describes
 CC osteoprotegerin (OPG) binding protein. Host cells transfected with
 CC vectors containing nucleic acid molecules encoding OPG binding protein
 CC are used to produce recombinant OPG binding protein. OPG binding protein
 CC is used in binding assays to determine osteoprotegerin (OPG) in biological
 CC samples; to screen for specific binding agents (particularly agonists
 CC and antagonists), including intracellular proteins; to raise Ab (useful
 CC in immunoassays for detection of OPG binding protein) and to identify
 CC compounds that modulate binding of OPG binding protein to ODA. The
 CC nucleic acid molecule encoding OPG binding protein can be used to detect
 CC OPG binding protein-encoding sequences, e.g. screening for related
 CC sequences, also to produce transgenic animal models, while complementary
 CC sequences are used for antisense regulation of OPG binding protein
 CC expression. Modulators of OPG binding protein, particularly soluble
 CC forms of OPG binding protein or Ab, are used to treat or prevent bone
 CC diseases, e.g. osteoporosis, bone loss caused by arthritis or
 CC metastases, hypercalcaemia, Paget's disease, periodontal disease,
 CC osteoporosis, loosening of prostheses, optionally in combination with
 CC agents that promote bone growth.

SQ Sequence 625 AA;

Query Match 3.2%; Score 9; DB 19; Length 625;
 Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 141 CKPWTNCTL 149
 |||||
 Db 170 ckpwtnctl 178

RESULT 21
 AAM69958
 ID AAM69958 standard; Protein: 625 AA.

AC AAM69958;

DT 08-OCT-1998 (first entry)

DE Murine NF-kB receptor activator mURANK.

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;
 KW immune response; inflammatory response; toxic shock; sepsis;
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; murine.

OS Mus sp.

PN WO9828426-A2.

PD 02-JUL-1998.

PF 22-DEC-1997; 97WO-US23775.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

PA (IMMV) IMMUNEX CORP.

PI Anderson DM, Gallibert LJ, Maraskovsky E;

DR WPI: 1998-377657/32.

DR N-PSDB; AAV41379.

PT New isolated ligand for receptor activator of NF-kappa B - used to
 PT develop products for augmenting an immune response for inhibiting an
 PT inflammatory response and for protection of cells

PS Example 14; Pages 62-64; 80pp; English.

XX This represents the murine mURANK (receptor activator of necrosis
 CC factor-kappa B (NF-kB)) polypeptide which is a homolog of the human RANK.
 CC RANK is a member of the tumour necrosis factor (TNF) family. A soluble
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell
 CC expressing membrane-associated RANK with a soluble RANK which binds to
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be
 CC used to induce maturation of dendritic cells and enhance their
 CC allo-stimulatory capacity, thereby augmenting an immune response. The
 CC soluble RANK polypeptide composition may also be used for regulating an
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists
 CC may be useful in ameliorating negative effects of an inflammatory
 CC response that result from triggering of RANK, e.g. in treating toxic
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory
 CC reactions. They can also be used in adjunct therapy for disease
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides
 CC can also be used to identify inhibitors of RANK and thus inhibitors of
 CC an inflammatory response, and also for protecting RANK-expressing cells
 CC from the negative effects of chemotherapy or the presence of high levels
 CC of TNF-alpha. The products can also be used for detection and drug
 CC screening.

SQ Sequence 625 AA;

Query Match 3.2%; Score 9; DB 19; Length 625;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149
 ID |||||||
 DB 170 ckpwtnctl 178

RESULT 22

AAW68294
 ID AAW68294 standard; Protein: 625 AA.

AC AAW68294;

DT 08-OCT-1998 (first entry)

DE Murine NF-kB receptor activator murANK.

KM RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KM Immune response; inflammatory response; toxic shock; sepsis;

KM RANKL; RANK ligand; tumour necrosis factor; TNF; murine.

OS Mus sp.

PN WO9828424-A2.

PD 02-JUL-1998.

PF 22-DEC-1997; 97WO-US23866.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

PA (IMV) IMMUNEX CORP.

PI Anderson DM, Gallibert LJ, Maraskovsky E;

DR WPI: 1998-377655/32.

DR N-PSDB; AAV41373.

PT New isolated receptor activator of necrosis factor-kappa B - useful
 for, e.g. developing products for regulating an immune or
 inflammatory response, treating toxic shock or sepsis

PS Claim 27; Pages 62-64; 80pp; English.

CC This represents the murine murANK (receptor activator of necrosis
 factor-kappa B (NF-kB)) polypeptide which is a homolog of the human RANK.
 CC RANK is a member of the tumour necrosis factor (TNF) family. Host cells
 CC transformed or transfected with an expression vector comprising the RANK
 CC encoding nucleic acid can be used to produce recombinant RANK protein.
 CC The soluble RANK may be used for inhibiting activation of NF-kB, by
 CC contacting a cell expressing membrane-associated RANK with a soluble
 CC RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide
 CC composition may also be used for regulating an immune or inflammatory
 CC response. Inhibition of NF-kB by RANK antagonists may be useful in
 CC ameliorating negative effects of an inflammatory response that result
 CC from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-
 CC versus-host reactions, or acute inflammatory reactions. They can also be
 CC used in adjunct therapy for disease characterised by neoplastic cells
 CC that express RANK. The products can also be used for detection and drug
 CC screening.

SO Sequence 625 AA;

Query Match 3.2%; Score 9; DB 19; Length 625;

Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149
 ID |||||||
 DB 170 ckpwtnctl 178

RESULT 23

AAV59509
 ID AAV59509 standard; Protein: 625 AA.

AC AAV59509;

DT 31-MAR-2000 (first entry)

DE OBM binding protein sequence.

KM OBM-BP; OBM binding protein; osteoclast formation promoting factor;

KM bone metabolic disease; osteoporosis; therapy.

OS Mus sp.

PN JP1332581-A.

PD 07-DEC-1999.

PF 20-OCT-1998; 98JP-0316973.

PR 24-MAR-1998; 98JP-0076232.

PA (SNOW) SNOW BRAND MILK PROD CO LTD.

PA (SANT) SANKYO CO LTD.

DR WPI: 2000-091362/08.

DR N-PSDB; AA249023.

PT A new protein, a DNA and its application -

PS Claim 10; Page 15-16; 18pp; Japanese.

CC This sequence is the osteoclast formation promoting factor (OBM)
 CC binding protein (OBM-BP) of the invention. The protein is useful as a
 CC preventive and/or treating agent for bone metabolic diseases such as
 CC osteoporosis. Substances which inhibit the binding of OBM to OBM-BP can
 CC be used as biochemical reagents.

SO Sequence 625 AA;

Query Match 3.2%; Score 9; DB 21; Length 625;

Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149
 ID |||||||
 DB 170 ckpwtnctl 178

RESULT 24

AAV53649
 ID AAV53649 standard; Protein: 625 AA.

AC AAV53649;

DT 22-FEB-2000 (first entry)

DE A mouse receptor activator of NF-kappaB designated RANK.

DE Mouse; receptor; RANK; Receptor activator of NF-kappaB;

KW osteoclast activity; immune response; inflammatory response;

KW excess bone resorption; osteoclast generation; bone loss; osteoporosis;

KW Paget's disease; bone cancer; cancer; hypercalcaemia; osteoclastogenesis;

KW metastasising cancer; osteoclast differentiation; signal transduction.

OS Mus sp.

PN WO958674-A2.

PD 18-NOV-1999.

XX 13-MAY-1999; 99MO-US10588.
XX 14-MAY-1998; 98US-0085487.
PR 03-DEC-1998; 98US-0110836.
XX (1MMV) IMMUNEX CORP.
XX
PI Anderson DM, Galibert LJ;
XX WPI: 2000-033099/04.
DR N-PSDB: AAZ36258.
XX
PT Novel cytokine receptors for regulating osteoclast activity to
PT ameliorate excess bone loss effects of osteoporosis, Paget's disease,
PT bone cancers etc
XX
PS Disclosure; Page 25-27; 28pp; English.
XX
CC The present sequence represents a soluble murine receptor designated RANK
CC (Receptor activator of NF-kappaB). The protein is used to regulate
CC osteoclast activity. The RANK protein or its fragments are useful for
CC regulating an immune or inflammatory response, especially to decrease
CC excess bone resorption, and for inhibiting osteoclast activity,
CC regulating osteoclast generation and inhibiting osteoclast generation
CC in individuals afflicted with excess bone resorption. Especially, the
CC RANK protein is used to treat individuals at risk for excess bone loss,
CC osteoporosis, Paget's disease, bone cancer and cancers associated with
CC hypercalcemia. The RANK protein ameliorates the effects of excess bone
CC loss, by binding to its ligand and inhibiting binding of other cells
CC into metastasizing cancers such as breast cancer, multiple myeloma,
CC melanomas, lung cancer, prostate, hematologic, head and neck, and renal
CC which metastasize to bone and induce bone breakdown by locally disrupting
CC normal bone remodeling, by disrupting the osteoclast differentiation
CC pathway. This results in the reduction in the number of osteoclasts,
CC lesser bone resorption and relief from the negative effects of
CC hypercalcemia. The RANK protein also ameliorates systemic effects by
CC interfering with I/I signal transduction that leads to the
CC differentiation of osteoclast precursors into osteoclasts.
XX
SQ Sequence 625 AA:

Query Match 3.2%; Score 9; DB 21; Length 625;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 CKPWTNCTL 149
Db 170 ckpwntctl 178

RESULT 25
AAE08739
ID AAE08739 standard; Protein: 625 AA.
XX
XX AAE08739:
DT 15-NOV-2001 (first entry)
XX
XX Murine receptor activator of NF kappaB (RANK) protein.
XX
XX Murine; receptor activator of nuclear factor kappaB; RANK; NF;
XX tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;
XX immune response; inflammatory response; graft-versus-host reaction;
XX toxic shock; sepsis; acute inflammatory reaction; bone resorption;
XX anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.
OS Mus sp.
XX
XX
FH Key Location/Qualifiers
FT Peptide 1..30

FT /label= signal_peptide
FT Protein 31..625
FT /label= Mature_RANK_protein
XX
XX US6271349-B1.
XX
XX 07-AUG-2001.
XX
XX
XX 17-DEC-1998; 98US-0215649.
XX
XX 23-DEC-1996; 96US-0059978.
XX 07-MAR-1997; 97US-0077181.
XX 14-OCT-1997; 97US-0064671.
XX 23-DEC-1996; 96US-0772330.
XX 07-MAR-1997; 97US-0813509.
XX 22-DEC-1997; 97US-0996139.
XX
XX (1MMV) IMMUNEX CORP.
XX
XX
XX Dougall WC, Galibert L;
XX WPI: 2001-520313/57.
XX N-PSDB: AAD15312.
XX
XX New receptor activator of NF-kappaB (RANK) polypeptides, useful for
XX regulating immune response, in screening for RANK inhibitors, or as an
XX adjunct therapy for disease characterized by neoplastic cells that
XX express RANK
XX
XX Example 14; Column 77-80; 47pp; English.
XX
XX The patent discloses novel receptor activator of nuclear factor (NF)-
XX kappaB (RANK) proteins and their corresponding DNAs. RANK is a member
XX of the tumour necrosis factor (TNF) receptor superfamily and associates
XX with TNF receptor associated factor (TRAF) 2 and 3 which are important
XX in the regulation of immune and inflammatory response. The receptors
XX are useful for regulating immune response and in screening for inhibitors
XX of these receptors. The cytoplasmic domain of RANK is used in developing
XX assays for inhibitors of signal transduction, e.g. for screening the
XX molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,
XX TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists
XX are useful in ameliorating the negative effects of an inflammatory
XX response that result from triggering of RANK, e.g. in treating toxic
XX shock or sepsis, graft-versus-host reactions, acute inflammatory
XX reactions and the effects of bone resorption. RANK acts as an anti-
XX apoptotic signal and rescue the cells that express RANK from apoptosis.
XX Soluble forms of the receptor are used in vivo or in vitro based
XX screening tests for agonists or antagonists of RANK activity, as
XX antagonists of RANK-mediated NF-kappa B activation, or to inhibit
XX transduction of a signal via RANK. RANK compositions are used in the
XX development of both agonistic and antagonistic antibodies, or as an
XX adjunct therapy for disease characterized by neoplastic cells that
XX express RANK. Compounds that interfere with RANK/TRAF6 interactions
XX are useful for modulating the formation of osteoclasts from osteoclast
XX precursors and for modulating osteoclast function and activities. They
XX are used as inhibitors of diseases associated with excess bone resorption
XX and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are
XX useful for the expression of recombinant proteins, as probes for analysis
XX of the presence or distribution of RANK transcripts, while the proteins
XX are useful in preparing kits for the detection of soluble RANK, or
XX monitor RANK-related activity. The present sequence is RANK protein
XX from murine.
XX
SQ Sequence 625 AA:

Query Match 3.2%; Score 9; DB 22; Length 625;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 141 CKPWTNCTL 149
Db 170 ckpwntctl 178

```

RESULT 26
AAE04427
ID AAE04427 standard; Protein; 625 AA.
XX
XX AAE04427;
AC
XX
XX
XX
XX 04-SEP-2001 (first entry)
DE Murine receptor activator of NF- $\kappa$ B (murANK) protein.
XX
XX Murine; receptor activator of NF- $\kappa$ B; RANK; tumour necrosis factor;
KM CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
KM chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.
XX
XX Mus sp.
OS
XX
XX
XX Key Location/Qualifiers
XX Region 197..214
XX FT /note="Spacer region"
XX
XX
XX US6242213-B1.
XX
XX PD 05-JUN-2001.
XX
XX PF 22-DEC-1997; 97US-0995659.
XX
XX PR 23-DEC-1996; 96US-0059978.
XX PR 07-MAR-1997; 97US-0077181.
XX PR 14-OCT-1997; 97US-0064671.
XX
XX PA (IMNV ) IMMUNEX CORP.
XX
XX PI Anderson DM;
XX
XX DR WPI: 2001-407216/43.
XX DR N-PSDB: AAD08716.
XX
XX PT New DNA molecules, useful for producing ligands (which are useful for
XX PT regulating immune response and in screening for inhibitors of NF- $\kappa$ B
XX PT receptor activator) of the receptor activator of NF- $\kappa$ B (RANK) -
XX
XX PS Example 14; Column 71-74; 43pp; English.
XX
XX CC The present invention relates to receptor activator of NF- $\kappa$ B (RANK)
XX CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
XX CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane-
XX CC proteins respectively. RANK is a member of the tumour necrosis factor
XX CC (TNF) superfamily and it closely resembles CD40. In the extracellular
XX CC region, RANK associates with TNF receptor-associated factor (TRAF) 2
XX CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
XX CC The ligands are useful for regulating immune response and in screening
XX CC for inhibitors of RANK. The present sequence is murine RANK
XX CC (murANK) protein.
XX
XX SQ Sequence 625 AA;

```

```

Query Match 3.2%; Score 9; DB 22; Length 625;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 141 CRPWTNCTL 149
DB 170 ckpwtncntl 178

```

```

RESULT 27
AAE01994
ID AAE01994 standard; Protein; 625 AA.
XX
XX AAE01994;
AC

```

```

XX
XX 31-JUL-2001 (first entry)
DE
XX
XX Murine RANK (receptor activator of NF- $\kappa$ B) protein.
XX
XX Mouse; receptor activator of NF- $\kappa$ B; RANK; nuclear factor- $\kappa$ B;
KM NF- $\kappa$ B; tumour necrosis factor; TNF; type I transmembrane protein;
KM TNF receptor-associated factor; TRAF; RANK ligand; RANKL; osteopetrotic;
KM inflammatory reaction; bone resorption; gene therapy; immunomodulator;
KM immune system dysfunction; familial expansile osteolysis; FEO;
XX early onset Paget's disease of bone; EP; cytostatic.
XX
XX Mus musculus.
OS
XX
XX
XX Key Location/Qualifiers
XX Region 197..214
XX FT /label= Spacer_Region
XX
XX
XX WO200136637-A1.
XX
XX PD 25-MAY-2001.
XX
XX PF 14-NOV-2000; 2000WO-US31459.
XX
XX PR 17-NOV-1999; 99US-0442029.
XX
XX PA (IMNV ) IMMUNEX CORP.
XX
XX PI Anderson DM, Hughes AE;
XX
XX DR WPI: 2001-329222/34.
XX DR N-PSDB: AAD05905.
XX
XX PT New DNA encoding a receptor activator of NF- $\kappa$ B polypeptide for the
XX PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
XX PT
XX PS Example 14; Page 80-82; 96pp; English.
XX
XX CC The present invention relates to a novel receptor, referred to as RANK
XX CC (receptor activator of NF (nuclear factor)- $\kappa$ B), a member of TNF
XX CC (tumour necrosis factor) receptor superfamily. RANK is a type I
XX CC transmembrane protein that interacts with TNF receptor-associated
XX CC factors (TRAFs). Triggering of RANK by overexpression or co-expression
XX CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation
XX CC of the transcription factor NF- $\kappa$ B, a ubiquitous transcription factor
XX CC that is most extensively utilised in cells of the immune system.
XX CC Inhibition of NF- $\kappa$ B by RANK antagonists is useful in ameliorating
XX CC negative effects of inflammatory reactions, and the effects of excess
XX CC bone resorption. The RANK DNAs, proteins and their analogues are useful
XX CC for the preparation of pharmaceutical compositions, for infecting target
XX CC cells for use in gene therapy applications in diagnosing diseases
XX CC associated with RANK, and as targets for use in screening assays. They
XX CC may be used in the treatment or diagnosis of immune system dysfunction.
XX CC The present invention also encompasses gene therapy methods to correct
XX CC gene-activating mutations, associated with e.g. familial expansile
XX CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
XX CC present amino acid sequence is murine RANK (murANK) protein. This
XX CC sequence which is a type I transmembrane protein contains a predicted 30
XX CC amino acid signal sequence, a 184 amino acid extracellular domain, a 21
XX CC amino acid transmembrane domain and a 390 amino acid cytoplasmic tail.
XX
XX SQ Sequence 625 AA;

```

```

Query Match 3.2%; Score 9; DB 22; Length 625;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY 141 CRPWTNCTL 149
DB 170 ckpwtncntl 178

```

```

RESULT 28
AAV44302
ID AAV44302 standard; Protein; 2126 AA.
XX
AC AAV44302;
XX
DT 29-FEB-2000 (first entry)
XX
DE Mouse acrosome reaction protein-PKDREJ.
XX
KM Acrosome reaction protein; P3; sperm protein; polycystin-1; sureJ;
KM Polycystic Kidney Disease and Receptor for Egg Jelly protein; PKDREJ;
KM zona pellucida; fertility; contraceptive; gene therapy; mouse.
XX
OS Mus musculus.
XX
PN WO9964457-A1.
XX
PD 16-DEC-1999.
XX
PF 10-JUN-1999; 99WO-GH01839.
XX
PR 10-JUN-1998; 98GB-0012534.
XX
PA (MED1-) MEDICAL RES COUNCIL.
XX
PI Harris PC, Hugues JR, Ward CJ;
XX
DR WPI; 2000-097518/08.
XX
DR N-PSDB; AAZ29336.
XX
PT New functional mammalian acrosome reaction protein, useful for
PT fertility treatment -
XX
PS Claim 1; Fig 2; 40pp; English.
XX
CC The present sequence is a functional mouse acrosome reaction protein,
CC PKDREJ or P3. PKDREJ is a sperm protein involved in binding the sperm
CC to the egg and/or triggering the acrosome reaction. It exhibits
CC homology to human polycystin-1 and sureJ. It can be used to
CC identify antibodies or proteins that block the acrosome reaction and
CC compounds that trigger acrosome reaction in the absence of zona
CC pellucida. Molecules that enhance the efficacy of the acrosome reaction
CC protein can be used to increase fertility and those blocking its
CC action can be used as contraceptives. DNA encoding PKDREJ can be used in
CC gene therapy and also as primer or probe for identifying sequences that
CC encode mutant forms of acrosome reaction protein.
XX
SQ Sequence 2126 AA;

Query Match 3.2%; Score 9; DB 21; Length 2126;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ALLLGLGL 23
Db 6 allllglgl 14

RESULT 29
ABG01304
ID ABG01304 standard; Protein; 51 AA.
XX
AC ABG01304;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #1295.
XX
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX

```

```

OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSEQ-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS65491.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX
PS Claim 20; SEQ ID NO 31663; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on human
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 51 AA;

Query Match 2.9%; Score 8; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLGLGL 23
Db 22 llllglgl 29

RESULT 30
ABG18404
ID ABG18404 standard; Protein; 51 AA.
XX
AC ABG18404;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #18395.
XX
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.

```

```

XX WO200175067-A2.
PN
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS82591.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID No 48763; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 51 AA;

```

```

Query Match          2.9%: Score 8; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 16 LLLLLGL 23
   |||||
   22 LLLGL 29

```

Search completed: June 18, 2002, 14:29:26
Job time: 219 sec